STIC Search Report
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STIC Database Tracking Number: 187330

TO: Marcela Cordero Garcia **Location: 3a30 / 3c18** **Art Unit: 1654** **Wednesday, April 26, 2006** **Case Serial Number: 10/722843**	**From: Noble Jarrell** **Location: Biotech-Chem Library** **Rem 1B71** **Phone: 272-2556** **Noble.jarrell@uspto.gov**

Search Notes

ACCESS DB # 187330

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: MARCELA M CORDERO GARCIA Examiner # : 80381 Date: 4/20/06
Art Unit: 1654 Phone Number: 2-2939 Serial Number: 10/722,843
Location (Bldg/Room#): REM3A30 (Mailbox #): REM3C18 Results Format Preferred (circle): PAPER DISK
****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Date: _____

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Searcher Location: _____
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Date Completed: 4/26/06
Searcher Prep & Review Time: 60
Online Time: 16

Type of Search

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_____ AA Sequence (#)
1 Structure (#)
✓ Bibliographic
_____ Litigation
_____ Fulltext
_____ Other

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✓ STN _____ Dialog
_____ Questel/Orbit _____ Lexis/Nexis
_____ Westlaw _____ WWW/Internet

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___ Commercial ___ Oligomer ___ Score/Length
___ Interference ___ SPDI ___ Encode/Transl
_____ Other (specify)

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L14          156 SEA FILE=REGISTRY ABB=ON  PLU=ON  PHSCN/SQSP


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FILE LAST UPDATED: 25 Apr 2006  (20060425/ED)

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 substance identification.
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=> d bib abs fhitseq hitrn retable l17 tot

L17 ANSWER 1 OF 3 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:610128 HCAPLUS
DN 141:157478
TI Peptides which target tumor and endothelial cells, compositions and uses thereof
IN **Allan, Amy L.**; Yoon, Won Hyung; **Gladstone, Patricia L.**; **Ternansky, Robert J.**; **Parry, Graham**; **Donate, Fernando**; **Mazar, Andrew**
PA **Attenuon, Llc, USA**
SO PCT Int. Appl., 117 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2004063213	A2	20040729	2003WO-US37895	20031125 <--
WO2004063213	A3	20050303		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA---2506813	AA	20040729	2003CA-2506813	20031125 <--
US2004162239	A1	20040819	2003US-0723144	20031125 <--
US2005020810	A1	20050127	2003US-0722843	20031125 <--
EP---1569678	A2	20050907	2003EP-0796483	20031125 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
BR2003016550	A	20051004	2003BR-0016550	20031125 <--
NO2005003112	A	20050805	2005NO-0003112	20050624 <--
PRAI 2002US-429174P	P	20021125 <--		
2003US-475539P	P	20030602 <--		
2003WO-US37895	W	20031125		

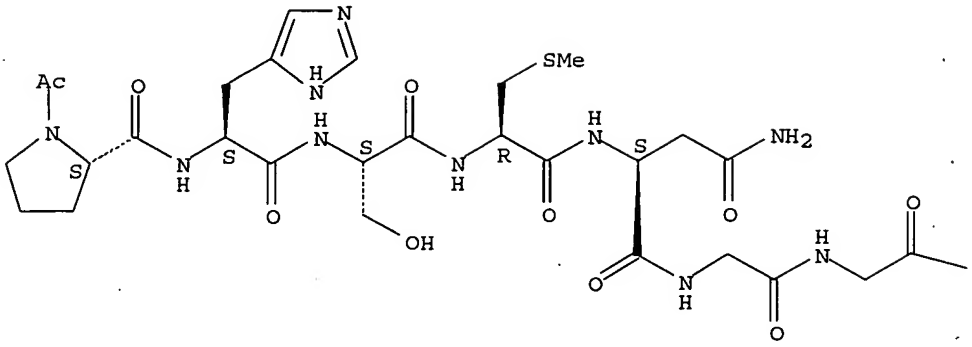
OS MARPAT 141:157478
AB The invention relates generally to peptide analogs of Ac-PHSCN-NH2 which target tumor and endothelial cells and have antitumor, antiangiogenic and antimetastatic activity and to methods for their synthesis and use in pharmaceutical compns. for treating, preventing and detecting diseases characterized by tumor growth, metastasis and angiogenesis. The peptide analogs may serve, inter alia, as carriers of radioactivity, PET-active compds., toxins, fluorescent mols. and PEG mols. Peptides R1[(NHCHR2CO)0-1(X1)0-100]m-X2-X3-X4-X5-X6-[(X7)0-1(NHCHR3CO)0-1]nNR4R5 [R1 is (un)substituted acyl, alkyl, cycloalkyl or imino, or acyl chelate; R2 is substituted alkyl; R4, R5 are (un)substituted alkyl; X1, X7 are NH(CH:CH)1-6CO, NH(CH2)1-6CO, NHCHMeCO; X2-X6 are α-amino acids which are defined; m, n are 0 or 1, with the proviso that R1 is not acetyl when R4 and R5 are H and m and n are 0] are claimed. Thus, Ac-Pro-His-Ser-Cys(Ac)-Asn-OH was prepared by the solid-phase method and coupled to doxorubicin hydrochloride to afford the conjugate.
IT **729594-60-9P**
RL: DGN (Diagnostic use); PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(preparation of peptides which target tumor and endothelial cells)
RN 729594-60-9 HCAPLUS
CN L-Lysinamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-S-methyl-L-cysteinyl-L-asparaginylglycylglycyl- (9CI) (CA INDEX NAME)

NTE modified

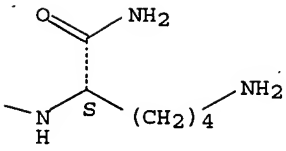
SEQ 1 PHSCNGGK

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IT INDEXING IN PROGRESS
IT 729594-60-9P
RL: DGN (Diagnostic use); PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(preparation of peptides which target tumor and endothelial cells)
IT 262438-43-7DP, analogs 729594-61-0P 729594-62-1P
729594-63-2P 729594-64-3P 729594-65-4P
729594-66-5P 729594-67-6P 729594-68-7P
729594-69-8P 729594-70-1P 729594-71-2P
729594-72-3P 729594-73-4P 729594-74-5P
729594-75-6P 729594-76-7P 729594-77-8P
729594-78-9P 729594-79-0P 729594-80-3P
729594-81-4P 729594-82-5P 729594-83-6P
729594-84-7P 729594-85-8P 729594-86-9P
729594-87-0P 729594-88-1P 729594-89-2P
729594-90-5P 729594-91-6P 729594-92-7P
729594-93-8P 729594-94-9P 729594-95-0P
729594-96-1P 729594-97-2P 729594-98-3P
729594-99-4P 729595-00-0P 729595-01-1P
729595-02-2P 729595-04-4P 729595-05-5P
729595-06-6P 729595-07-7P 729595-08-8P

729595-09-9P 729595-14-6P 730960-54-0P
731003-01-3DP, Indium complexes 731003-01-3P
731003-02-4P
RL: DGN (Diagnostic use); PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(preparation of peptides which target tumor and endothelial cells)

IT 729595-16-8D, resin-bound 729595-17-9
RL: RCT (Reactant); RACT (Reactant or reagent)
(preparation of peptides which target tumor and endothelial cells)

IT 729595-10-2DP, resin-bound 729595-11-3DP, resin-bound
729595-12-4DP, resin-bound 729595-13-5DP, resin-bound
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(preparation of peptides which target tumor and endothelial cells)

L17 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:467702 HCAPLUS
DN 141:33798
TI Peptides which inhibit angiogenesis, cell migration, cell invasion and cell proliferation, their preparation, and compositions and therapeutic uses thereof
IN **Allan, Amy L.**; **Donate, Fernando**; Hopkins, Stephanie A.; **Gladstone, Patricia L.**; **Mazar, Andrew**; O'Hare, Sean M.; **Parry, Graham**; Plunkett, Marian L.; **Ternansky, Robert J.**; Yoon, Won Hyung
PA **Attenuon, LLC, USA**
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2004047771	A2	20040610	2003WO-US38175	20031125 <--
WO2004047771	A3	20050915		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA---2507045	AA	20040610	2003CA-2507045	20031125 <--
US2004162239	A1	20040819	2003US-0723144	20031125 <--
US2005020810	A1	20050127	2003US-0722843	20031125 <--
BR2003016523	A	20051018	2003BR-0016523	20031125 <--
EP---1594521	A2	20051116	2003EP-0812058	20031125 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
NO2005003111	A	20050824	2005NO-0003111	20050624 <--
PRAI 2002US-429174P	P	20021125	<--	
2003US-475539P	P	20030602	<--	
2003WO-US38175	W	20031125		

OS MARPAT 141:33798
AB The invention discloses peptides which inhibit angiogenesis, cell migration, cell invasion and cell proliferation, as well as methods of making the peptides, pharmaceutical compns. containing the peptides, and methods of using the peptides and pharmaceutical compns. to treat diseases associated with aberrant vascularization, e.g. cancer.

IT 701200-82-0P
RL: PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP

(Preparation); RACT (Reactant or reagent); USES (Uses)
(peptide inhibitors of angiogenesis, cell migration, cell invasion and cell proliferation, preparation, and compns. and therapeutic uses)

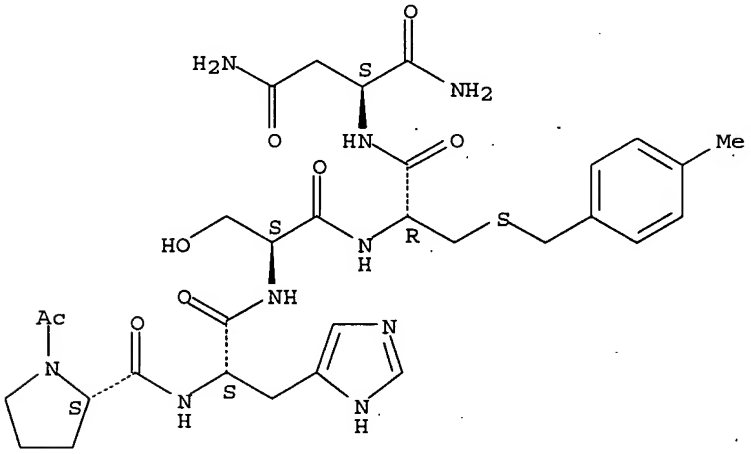
RN 701200-82-0 HCAPLUS

CN L-Aspartamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-S-[(4-methylphenyl)methyl]-L-cysteinyl- (9CI) (CA INDEX NAME)

NTE modified

SEQ 1 PHSCN

Absolute stereochemistry.



IT INDEXING IN PROGRESS

IT **701200-82-0P 701201-01-6P**
RL: PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(peptide inhibitors of angiogenesis, cell migration, cell invasion and cell proliferation, preparation, and compns. and therapeutic uses)

IT **701200-81-9P 701200-88-6P 701200-90-0P**
701200-91-1P 701200-92-2P 701200-93-3P
701200-99-9P 701201-02-7P 701201-03-8P
701201-04-9P 701201-05-0P 701201-06-1P
701201-07-2P 701201-08-3P 701201-09-4P
701201-10-7P 701201-11-8P 701201-12-9P
701201-13-0P
RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(peptide inhibitors of angiogenesis, cell migration, cell invasion and cell proliferation, preparation, and compns. and therapeutic uses)

IT **262438-43-7**
RL: RCT (Reactant); RACT (Reactant or reagent)
(peptide inhibitors of angiogenesis, cell migration, cell invasion and cell proliferation, preparation, and compns. and therapeutic uses)

L17 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:243058 HCAPLUS

DN 139:173332

TI Inhibition of integrin α5β1 function with a small peptide (ATN-161) plus continuous 5-FU infusion reduces colorectal liver metastases and improves survival in mice

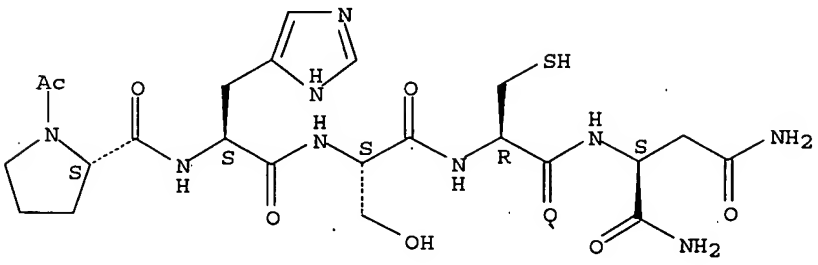
AU Stoeltzing, Oliver; Liu, Wenbiao; Reinmuth, Niels; Fan, Fan; **Parry, Graham C.**; Parikh, Alexander A.; McCarty, Marya F.; Bucana, Corazon

D.; Mazar, Andrew P.; Ellis, Lee M.
CS Department of Cancer Biology, The University of Texas M.D. Anderson Cancer Center, Houston, TX, 77030-4009, USA
SO International Journal of Cancer (2003), 104(4), 496-503
CODEN: IJCNAW; ISSN: 0020-7136
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Integrin α5β1 is expressed on activated endothelial cells and plays a critical role in tumor angiogenesis. We hypothesized that a novel integrin α5β1 antagonist, ATN-161, would inhibit angiogenesis and growth of liver metastases in a murine model. We further hypothesized that combining ATN-161 with 5-fluorouracil (5-FU) chemotherapy would enhance the antineoplastic effect. Murine colon cancer cells (CT26) were injected into spleens of BALB/c mice to produce liver metastases. Four days thereafter, mice were given either ATN-161 (100 mg/kg, every 3rd day) or saline by i.p. injection, with or without combination of continuous-infusion 5-FU (100 mg/kg/2 wk), which was started on day 7. On day 20 after tumor cell inoculation, mice were killed and liver wts. and number of liver metastases were determined A follow-up study on survival was also conducted in which mice were randomized to receive ATN-161, 5-FU or ATN-161+5-FU. Combination therapy with ATN-161+5-FU significantly reduced tumor burden (liver weight) and number of liver metastases ($p<0.02$). Liver tumors in the ATN-161 and ATN-161+5-FU groups had significantly fewer microvessels ($p<0.05$) than tumors in the control or 5-FU-treated groups. Unlike treatment with either agent alone, ATN-161+5-FU significantly increased tumor cell apoptosis and decreased tumor cell proliferation ($p<0.03$) and improved overall survival ($p<0.03$, log-rank test). Targeting integrin α5β1 in combination with 5-FU infusion reduced liver metastases formation and improved survival in this colon cancer model. The enhancement of antineoplastic activity from the combination of anti-angiogenic therapy and chemotherapy may be a promising approach for treating metastatic colorectal cancer.
IT **262438-43-7**, ATN 161
RL: DMA (Drug mechanism of action); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(inhibition of integrin α5β1 function with ATN-161 plus 5-FU infusion reduces colorectal liver metastases and improves survival in mice)
RN 262438-43-7 HCAPLUS
CN L-Aspartamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

NTE modified

SEQ 1 PHSCN

Absolute stereochemistry.



IT INDEXING IN PROGRESS
IT **262438-43-7**, ATN 161
RL: DMA (Drug mechanism of action); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(inhibition of integrin α5β1 function with ATN-161 plus 5-FU infusion reduces colorectal liver metastases and improves survival in mice)

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Baker, C	2002	62	1996	Cancer Res	HCAPLUS
Bello, L	2001	61	7501	Cancer Res	HCAPLUS
Bergsland, E	2000	19	242	Proc Am Soc Clin Onc	
Braakhuis, B	1995	22	42	Semin Oncol	HCAPLUS
Brooks, P	1994	79	1157	Cell	HCAPLUS
Brooks, P	1995	96	1815	J Clin Invest	HCAPLUS
Browder, T	2000	60	1878	Cancer Res	HCAPLUS
Bruns, C	2000	89	488	Cancer	HCAPLUS
Bruns, C	2000	6	1936	Clin Cancer Res	HCAPLUS
Fidler, I	1991	10	229	Cancer Metastasis Re	MEDLINE
Friedlander, M	1995	270	1500	Science	HCAPLUS
Gately, S	2001	7	427	Cancer J	MEDLINE
Giancotti, F	1999	285	1028	Science	HCAPLUS
Gong, J	1997	8	83	Cell Growth Differ	HCAPLUS
Griggs, D	2001	42	1420	Proc Am Assoc Cancer	
Hanahan, D	2000	105	1045	J Clin Invest	HCAPLUS
Hynes, R	1992	69	11	Cell	HCAPLUS
Kakeji, Y	1997	15	39	Invest New Drugs	HCAPLUS
Kase, S	1993	13	369	Anticancer Res	HCAPLUS
Kerbel, R	2002	13	12	Ann Oncol	MEDLINE
Kerbel, R	2000	36	1248	Eur J Cancer	HCAPLUS
Kerr, J	1999	19	959	Anticancer Res	HCAPLUS
Kerr, J	2000	9	1271	Expert Opin Investig	HCAPLUS
Kim, S	2000	156	1345	Am J Pathol	HCAPLUS
Kim, S	2000	275	33920	J Biol Chem	HCAPLUS
Klement, G	2002	8	221	Clin Cancer Res	HCAPLUS
Klement, G	2000	105	R15	J Clin Invest	HCAPLUS
Klotz, O	2000	238	88	Arch Clin Exp Ophtha	HCAPLUS
Kumar, C	2000	476	169	Adv Exp Med Biol	MEDLINE
Kumar, C	2001	61	2232	Cancer Res	HCAPLUS
Livant, D	2000	60	309	Cancer Res	HCAPLUS
Lode, H	1999	96	1591	Proc Natl Acad Sci U	HCAPLUS
Morikawa, K	1990	82	517	J Natl Cancer Inst	HCAPLUS
Mross, K	2000	3	223	Drug Resist Updat	HCAPLUS
O'Brien, V	1996	224	208	Exp Cell Res	HCAPLUS
Remmenga, S	1994	55	115	Gynecol Oncol	MEDLINE
Schreiner, C	1991	9	163	Clin Exp Metastasis	HCAPLUS
Stoeltzing, O	2001	7	3656S	Clin Cancer Res	
Storgard, C	1999	103	47	J Clin Invest	HCAPLUS
Tedjarati, S	2002	8	2413	Clin Cancer Res	HCAPLUS
Varner, J	1995	6	725	Mol Biol Cell	HCAPLUS
White, E	2001	167	5362	J Immunol	HCAPLUS

=> d bib abs hitseq retable l20 tot

L20 ANSWER 1 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:663850 HCAPLUS
DN 141:186005
TI Rice nucleic acid molecules and encoded proteins and their uses for plant improvement
IN La Rosa, Thomas J.; Kovalic, David K.; Zhou, Yihua; Cao, Yongwei; Wu, Wei; Boukharov, Andrey A.; Barbazuk, Brad W.
PA USA
SO U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 837,604. CODEN: USXXCO
DT Patent

LA English
FAN.CNT 27

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US2004123343	A1	20040624	2003US-0437963	20030514 <--
	US2004123343	A1	20040624	2003US-0437963	20030514 <--
PRAI	2000US-197872P	P	20000419 <--		
	2001US-0837604	A2	20010418 <--		
	2003US-0437963	A	20030514		

AB The present invention provides 102,483 cDNA sequences and their encoded protein sequences from rice (Oryza sativa). Bioinformatic anal. identified putative functions and uses for the nucleic acids/polypeptides. The disclosed polynucleotides and polypeptides find use in production of transgenic plants to produce plants having improved properties. [This abstract record is one of forty-one records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **736624-12-7**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; rice nucleic acid mols. and encoded proteins and their uses for plant improvement)

RN 736624-12-7 HCAPLUS
CN Protein (Oryza sativa clone PAT_MRT4530_75798C.1.pep fragment) (9CI) (CA INDEX NAME)

SEQ 1 SVPFLPAEIL TTWVSIPILS PMTLLLCSLF TWMKLEGFTV HATPHSCNHL
51 L

L20 ANSWER 2 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:663844 HCAPLUS
DN 141:186000
TI Rice nucleic acid molecules and encoded proteins and their uses for plant improvement
IN La Rosa, Thomas J.; Kovalic, David K.; Zhou, Yihua; Cao, Yongwei; Wu, Wei; Boukharov, Andrey A.; Barbazuk, Brad W.
PA USA
SO U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 837,604.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 27

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US2004123343	A1	20040624	2003US-0437963	20030514 <--
	US2004123343	A1	20040624	2003US-0437963	20030514 <--
PRAI	2000US-197872P	P	20000419 <--		
	2001US-0837604	A2	20010418 <--		
	2003US-0437963	A	20030514		

AB The present invention provides 102,483 cDNA sequences and their encoded protein sequences from rice (Oryza sativa). Bioinformatic anal. identified putative functions and uses for the nucleic acids/polypeptides. The disclosed polynucleotides and polypeptides find use in production of transgenic plants to produce plants having improved properties. [This abstract record is one of forty-one records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **736366-35-1**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; rice nucleic acid mols. and encoded proteins and their uses for plant improvement)

RN 736366-35-1 HCAPLUS
CN Protein (Oryza sativa clone PAT_MRT4530_52392C.1.pep fragment) (9CI) (CA INDEX NAME)

SEQ
```
   1 MAHTSGVAAR LNLVFMGRPL ARSAQPPPSG PRFSGRAQRR RGSNEATACG
  51 KGRSRAGRAA SPDVVATKPP PLHDEEEEEG GRMVRRGRKG KDAAAGAGGT
 101 GGRGGGAGRG GGRGGSGGGG GGGGVREATL VRVSKVLEDF QASDAQVYKF
 151 EPGISKQERA AIHEMCRKMG MISKSSGNGE RRCLSVYKRK QNQGLETEEG
 201 PSHLGFSVEA RNVLQDLFMH YPPDDAELNG HTVRNSSDKA VKIQWKPDGA
 251 FCRPALRKPD ILKKVEMLAS KIVQDRSKLP ISSYKDAISS TLENHQVVLI
 301 SGETGCGKTT QVPQYILDHM WGKGESCKIV CTQPRRISAI SVAERISAER
 351 GESVGDTVGY KIRLESKGGK NSSIMFCTNG VLLRLLIGRR IAENIYQLFL
 401 CNSERAEHLD EIHERDRFSD FMLAILRDLL PLYPHLRLVK TFYLEDVLSI
 451 LQSVGDNHLD PTTDDLKQSS LLTDDYKSSM DEAINLALDN DEFDPLLELI
 501 SAEQNQEIFN YQHSETGVTP LMVLAGKGQV GDICMLLSFG VDCSTRDHDG
 551 KSALGWAEQG NQQEVCEVIK KHMECGSAKL TEENELLNKY LATINPEHID
 601 TVLIERLLRK ICVDSNEGAI LVFLPGWEDI NQTRERLLAS PFFQDSSKFL
 651 VLSLHSMIPS SEQKKVFKRP PAGSRKIILS TNIAETAVTI DDVVFVIDSG
 701 RMKEKSYDPY NNVSTLHSSW VSKANARQRQ GRAGRCQPGT CYHLYSRFRA
 751 ASLLEYQIPE IKRMPIEELC LQVKLLDPNC RIADFLRKTL DPPIPETVRN
 801 AITVLQDLGA LTQDEQLTEL GEKLGSLPVH PSTSKMLLFG ILMNCLDPAL
 851 TLACAADYRD PFLLPMAPDE RKRAAAAKVE LASLYGGYSD QLAVVAAMDC
 901 WRRAKDRGQE AQFCSKYFVS SNTMNMLSNM RKQLQNELAQ RGFVPVDASA
 951 CSLNARDPGI IRAVLMAGAY PMVGRLLPPR KNTRRAVIET ASGAKVRLHP
1001 HSCNFNLSFR KTSGNPLVIY DEITRGDGGM YIKNSSVVGS YPLIILATEM
1051 VVAPPEDDDS DEEDGDSSED ETEKVTLGQH KEIMSSPDNS VSVVIDRWLR
1101 FDATALDVAQ IYCLRERLAS AILFKVKHPQ DVLPPDLGAT MYAIACILSY
1151 DGLPAMITSD DVATSQGSNQ SSAESSRFSQ GRRVGYIPPG GFLMSLLSDK
1201 PLNAPHFQKS FNHPDGASGH IRSSRTSVGR FDQSRHPQRN NSGPGSSAAR
1251 TFKRQRNGAQ
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L20 ANSWER 3 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:449883 HCAPLUS
DN 140:402911
TI Binary prediction tree modeling with many predictors and its uses in clinical and genomic applications
IN Nevins, Joseph R.; West, Mike; Huang, Andrew T.
PA Duke University, USA
SO PCT Int. Appl., 886 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2004038376	A2	20040506	2003WO-XA33946	20031024 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO2004038376	A2	20040506	2003WO-US33946	20031024 <--
WO2004038376	A3	20040826		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ,				

OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM,
TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI 2002US-420729P P 20021024 <--
2002US-421062P P 20021025 <--
2002US-421102P P 20021025 <--
2002US-424701P P 20021108 <--
2002US-424715P P 20021108 <--
2002US-424718P P 20021108 <--
2002US-425256P P 20021112 <--
2003US-448461P P 20030221
2003US-448462P P 20030221
2003US-457877P P 20030327
2003US-458373P P 20030331
2003WO-US33946 A 20031024

AB The statistical anal. described and claimed is a predictive statistical tree model that overcomes several problems observed in prior statistical models and regression analyses, while ensuring greater accuracy and predictive capabilities. Although the claimed use of the predictive statistical tree model described herein is directed to the prediction of a disease in individuals, the claimed model can be used for a variety of applications including the prediction of disease states, susceptibility of disease states or any other biol. state of interest, as well as other applicable non-biol. states of interest. This model first screens genes to reduce noise, applies kmeans correlation-based clustering targeting a large number of clusters, and then uses singular value decompns. (SVD) to extract the single dominant factor (principal component) from each cluster. This generates a statistically significant number of cluster-derived singular factors, that are referred to as metagenes, that characterize multiple patterns of expression of the genes across samples. The strategy aims to extract multiple such patterns while reducing dimension and smoothing out gene-specific noise through the aggregation within clusters. Formal predictive anal. then uses these metagenes in a Bayesian classification tree anal. This generates multiple recursive partitions of the sample into subgroups (the 'leaves' of the classification tree), and assocs. Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate wts., across many such tree models. The model includes the use of iterative out-of-sample, cross-validation predictions leaving each sample out of the data set one at a time, refitting the model from the remaining samples and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world prognostic context where prediction of new cases as they arise is the major goal.

IT **391964-05-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; binary prediction tree modeling with many predictors and its uses in clin. and genomic applications)

RN 391964-05-9 HCAPLUS

CN NFX1 (human cell line Raji clone NFX.1 cDNA #16) (9CI) (CA INDEX NAME)

SEQ
1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
151 KPKKATQFVY SYARGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDPEKCT
301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH

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  501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
  551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
  601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
  651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLNCG
  701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
  751 ECTQTCARVH ECDHPVYHSG HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
  801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
  851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
  901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
  951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
 1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
 1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
 1101 DVQD
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L20 ANSWER 4 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:369010 HCAPLUS
DN 140:369948
TI Nucleic acids encoding human polypeptides and their diagnostic and therapeutic uses
IN Williams, Lewis T.; Chu, Keting; Lee, Ernestine; Hestir, Kevin; Beaurang, Pierre Alvaro; Behrens, Dirk; Halenbeck, Robert Forgan; Kothakota, Srinivas; Lin, Haishan; Linnemann, Thomas; Pierce, Kristen; Wang, Yan; Wong, Justin G. P.; Wu, Ge; Zhang, Hongbing; Zeng, Changjiang
PA Five Prime Therapeutics, Inc., USA
SO PCT Int. Appl., 532 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 18

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO2004038003	A2	20040506	WO 2003-US33947	20031024 <--
	WO2004038003	A3	20041209		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU2003298606	A1	20040513	2003AU-0298606	20031024 <--
PRAI	2002US-421061P	P	20021025	<--	
	2002US-421080P	P	20021025	<--	
	2002US-421552P	P	20021025	<--	
	2002US-421614P	P	20021025	<--	
	2002US-422177P	P	20021030	<--	
	2002US-422178P	P	20021030	<--	
	2002US-426355P	P	20021115	<--	
	2002US-426384P	P	20021115	<--	
	2002US-426394P	P	20021115	<--	
	2002US-426430P	P	20021115	<--	
	2002US-426916P	P	20021115	<--	
	2002US-429224P	P	20021127	<--	
	2002US-429275P	P	20021127	<--	
	2002US-429302P	P	20021127	<--	
	2002US-429326P	P	20021127	<--	
	2002US-429651P	P	20021127	<--	
	2002US-430645P	P	20021204	<--	
	2002US-430651P	P	20021204	<--	
	2002US-430657P	P	20021204	<--	

2002US-430663P	P	20021204	<--
2002US-430668P	P	20021204	<--
2002US-430684P	P	20021204	<--
2002US-430937P	P	20021205	<--
2002US-430965P	P	20021205	<--
2002US-431458P	P	20021205	<--
2002US-433251P	P	20021212	<--
2002US-433500P	P	20021212	<--
2002US-433316P	P	20021213	<--
2002US-433318P	P	20021213	<--
2002US-436236P	P	20021223	<--
2003US-437914P	P	20030103	
2003US-440820P	P	20030117	
2003US-440821P	P	20030117	
2003US-463700P	P	20030418	
2003US-463708P	P	20030418	
2003US-463716P	P	20030418	
2003US-463732P	P	20030418	
2003US-467199P	P	20030502	
2003US-467201P	P	20030502	
2003US-467203P	P	20030502	
2003US-467230P	P	20030502	
2003US-471306P	P	20030519	
2003US-471336P	P	20030519	
2003US-472420P	P	20030522	
2003US-472430P	P	20030522	
2003US-476609P	P	20030609	
2003US-476621P	P	20030609	
2003US-476632P	P	20030609	
2003US-476641P	P	20030609	
2003US-485223P	P	20030708	

AB The invention provides 784 novel human cDNA sequences plus their encoded polypeptides and mouse homologs, and related modulators, such as antibodies and small mol. modulators. The invention also provides methods to make and use these polynucleotides, polypeptides, related compns., and modulators. These methods include diagnostic, prophylactic, and therapeutic applications. The compns. and methods of the invention are useful in treating proliferative disorders, e.g., cancers, and inflammatory, immune, bacterial, and viral disorders.

IT **683848-87-5**, Protein (human clone HG1013154.P1)
RL: ANT (Analyte); ARG (Analytical reagent use); DGN (Diagnostic use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids encoding human polypeptides and their diagnostic and therapeutic uses)

RN 683848-87-5 HCAPLUS

CN Protein (human clone HG1013154.P1) (9CI) (CA INDEX NAME)

SEQ
```
  1 MLEQKRDPWT LQSEVKIINN PDGRECIKGV NTEQKVHIRE KPYGCNEHGK
 51 VFRVSSSLTN RQVIHIADKT YKCSDCGEIF SSNSNFAQHQ RIHTGEKPYK
101 YNECGKVFNQ NSHLAQHQKI HTGQKPYNNK ECGKVFSHHA YLAQHRKIHT
151 GEKPYKCSEC GKAFSVCSSL TAHLVIHTGE KPYDCKECGK VFRHKSSLTT
201 HQTVHTGERP YKCNECGKGF SRIAFLARHR KVHTGEKPYK CNECGKVFIG
251 NSRLARHRKI HTGGRRYKCN ECGKAFRTCS DLTAHLLIHT GEKPYECIDC
301 GKVFRHKSSL TYHCRIHTGE KPYKCNECGK VFSQNSNLQR HRKIHTGEKL
351 YKCNECGKVF RQNSHLAQHR DIHTGEKPYS CNECGKVFRR NSHLVRHRNV
401 HTGEKPYSCN ECGKVFSRNS HLARHRNIHT GEKPHSCNEC GKVFSRNSHL
451 ARHRKIHTGE KLYKCNECSK VFSRNSRLAQ HRNIHTGVKP YSCNECGKVF
501 SKNSILVQHC SIHTREKP
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L20 ANSWER 5 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2004:209219 HCAPLUS

DN 140:230623
TI Soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement
IN La Rosa, Thomas J.; Zhou, Yihua; Kovalic, David K.; Cao, Yongwei
PA USA
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 76

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US2004031072	A1	20040212	2003US-0424599	20030428 <--
	US2004031072	A1	20040212	2003US-0424599	20030428 <--
PRAI	1999US-0304517	B1	19990506 <--		
	2001US-0985678	B2	20011105 <--		
	2003US-0424599	A	20030428		

AB This invention provides 142,842 polynucleotide sequences isolated from a cDNA library generated from Glycine maximum The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 72 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **666944-30-5**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement)
RN 666944-30-5 HCAPLUS
CN Transcription-associated protein (Glycine max clone PAT_MRT3847_136416C.1.pep fragment) (9CI) (CA INDEX NAME)

SEQ
```
  1 MAHLADLCQK LKVIEQCQVS PPPGSVPPTS LPLAFLDLPW VYCDTVQSIF
 51 FFEFPHSCNH FLQTVLPNLK HSLSLTLQQF FPFVGNLVIP PKPNFPHILY
101 TSENSISFTI AESTADFPHL IADTARDVKD SHPFVPILPT PTTKEDGTWL
151 LPLMAIQLTI FPEYGFSICI SFRHVVADAR AFLHFMKFWS YVCRTKHDVA
201 ATQDLLPLLN RDIIKDPKGL KFVSEELWNS PIESIIKT
```

L20 ANSWER 6 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:155817 HCAPLUS
DN 140:194470
TI Nucleic acids and encoded proteins associated with plants and their uses for plant improvement
IN Liu, Jingdong; Zhou, Yihua; Kovalic, David K.; Screen, Steven E.; Tabaska, Jack E.; Cao, Yongwei
PA USA
SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 76

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US2004034888	A1	20040219	2003US-0425114	20030428 <--

	US2004034888	A1	20040219	2003US-0425114	20030428 <--
PRAI	1999US-0304517	B1	19990506 <--		
	2001US-0985678	B2	20011105 <--		
	2003US-0425114	A	20030428		

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hirsutum, Cucumis sativis, Lilium asiatic, Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **661754-58-1**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and encoded proteins associated with plants and their uses for plant improvement)

RN 661754-58-1 HCAPLUS

CN Protein (Glycine max clone 700747514_FLI.pep fragment) (9CI) (CA INDEX NAME)

SEQ
```
  1 GQTEQKPNTP HSCNQSMAEP SSSKPAVPLL KDELDIVIPT IRNLDFLEMW
 51 RPFFEPYHLI IVQDGDPNRT IKVPDGFDYE LYNRNDINRI LGPKASCISF
101 KDSACRCFGY MVSKKKYIYT IDDDCFVAKD PSGKDINALE QHIKNLLCPS
151 TPFFFNTLYD PYRAGADFVR GYPFSLREGA PTAVSHGLWL NIPDYDAPTQ
201 LVKPLERNTR YVDAVLTIPK GTLFPMCGMN LAFDRQLIGP AMYFGLMGDG
251 QPIGRYDDMW AGWCVKVICD HLGLGVKTGL PYIWHSKASN PFVNLKKEYK
301 GIFWQEEIIP FFQSATIPKE CTSVQKCYIE LSKQVKEKLG AVDPYFTKLA
351 DAMVTWIEAW DELNSTTSEE ASSKSANGAA AATK
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L20 ANSWER 7 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2004:155810 HCAPLUS

DN 140:194467

TI Nucleic acids and encoded proteins associated with plants and their uses for plant improvement

IN Liu, Jingdong; Zhou, Yihua; Kovalic, David K.; Screen, Steven E.; Tabaska, Jack E.; Cao, Yongwei

PA USA

SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO

DT Patent

LA English

FAN.CNT 76

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US2004034888	A1	20040219	2003US-0425114	20030428 <--
	US2004034888	A1	20040219	2003US-0425114	20030428 <--
PRAI	1999US-0304517	B1	19990506 <--		
	2001US-0985678	B2	20011105 <--		
	2003US-0425114	A	20030428		

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum,

Brassica napus, Gossypium hirsutum, Cucumis sativis, Lilium asiatic, Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 661628-65-5
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and encoded proteins associated with plants and their uses for plant improvement)

RN 661628-65-5 HCAPLUS

CN Protein (Zea mays mexicana clone uC-zmroteosinte018g09_FLI.pep fragment) (9CI) (CA INDEX NAME)

SEQ
```
  1 LLIGRGTNAS KARNQKRSLD DAVLGITHII VDEIHERDRF SDFMLTILRD
 51 LLPLYPHLRM VLMSATIDAE RFSQYFNGCS VIQVPGFTYP VKSFYLEDVL
101 SILQSAEQNT EVYNYQHSET GITPLMVFAM KGQLGDVCML LSFGVDCSAQ
151 DHDGKSALDW AQQENQQEVC EVIKKHMECS SEKSTEDNEL LNKYLASINP
201 EHIDTLLIER LLRKICVDSN EGAILVFLPG WEDISQTRER LFASPFFQDS
251 SRFLVLSLHS MIPSSEQKKV FKRPPVGVRK IILSTNIAET AVTIDDVVFV
301 IDSGRMKEKS YDPYNNVSTL HASWVSKASA RQREGRAGRC QPGTCYHLYS
351 RFRASSLPDY QIPEIKRMPI EELCLQVKLL DSNCRIADFL KKTLDPPIPE
401 TVRNAIAVLQ DLGALTQDEQ LTELGEKLGS LPVHPSTTKM LLFAILMNCL
451 DPALTLACAA DYRDPFVLPV APDERKRAAA AKVELASLYG GFSDQLAVVA
501 AFDCWRHAKD RGQDSQFCAK YFVSSNIMNM LSSMRKQLQN ELSQRGFVPA
551 DASACSLNSK DPGIMRAVLM AGAYPMVGKM LPPRKNARKS VLETASGAKV
601 RLHPHSCNFN LSFSKSSGNP LLIYDEITRG DGGMYIKNSS VVGSYPLLLI
651 AAEMVVAPPD DDSDEDEEDS SEDEAEESTL VQHKEEIMSS PDSIVSVVVD
701 RWLRFDATAL DVAQIYCLRE RLASAILFKV KHPQDVLPPA LGASMYAITC
751 ILSFDGLPSM VPPNDLSANR GSGQDLAEAS KFSQGRRAGY IPPSGFLMSL
801 LADRTHNAPS FQNSSNHPGG GSAHTRPSRA PVGRFDRSRR PFRNSGPGSS
851 APRSFKRQRD APR
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L20 ANSWER 8 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:942764 HCAPLUS

DN 140:3792

TI Genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics

IN Nevins, Joseph; West, Mike; Goldschmidt, Pascal

PA Duke University, USA

SO PCT Int. Appl., 408 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO2003091391	A2	20031106	2002WO-XA38221	20021112 <--

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,

NE, SN, TD, TG
WO2003091391 A2 20031106 2002WO-US38221 20021112 <--
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP,
KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, UA, UG, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF,
CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRAI 2002US-374547P P 20020423 <--
2002US-420784P P 20021024 <--
2002US-421043P P 20021025 <--
2002US-424680P P 20021108 <--
2002WO-US38221 A 20021112 <--
AB Genes whose expression is correlated with an determinant of an atherosclerotic phenotype are provided. Also provided are methods of using the subject atherosclerotic determinant genes in diagnosis and treatment methods, as well as drug screening methods. In addition, reagents and kits thereof that find use in practicing the subject methods are provided. Also provided are methods of determining whether a gene is correlated with a disease phenotype, where correlation is determined using a Bayesian anal.
IT 391964-05-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics)
RN 391964-05-9 HCAPLUS
CN NFX1 (human cell line Raji clone NFX.1 cDNA #16) (9CI) (CA INDEX NAME)

SEQ
1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
151 KPKKATQFVY SYARGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDPEKCT
301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLNCG
701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
751 ECTQTCARVH ECDHPVYHSG HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
1101 DVQD

L20 ANSWER 9 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:913280 HCAPLUS
DN 139:379453
TI Genes showing altered patterns of expression in multiple sclerosis and their diagnostic and therapeutic uses
IN Dangond, Fernando; Hwang, Daehee

PA Brigham and Women's Hospital, Inc., USA
SO PCT Int. Appl., 148 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO2003095618	A2	20031120	2003WO-US14462	20030507 <--
	WO2003095618	A3	20041021		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US2004018522	A1	20040129	2003US-0430762	20030506 <--
	AU2003228936	A1	20031111	2003AU-0228936	20030507 <--
PRAI	2002US-379284P	P	20020509 <--		
	2003US-0430762	A1	20030506		
	2003WO-US14462	W	20030507		

AB The present invention identifies a number of gene markers whose expression is altered in multiple sclerosis (MS). These markers can be used to diagnose or predict MS in subjects, and can be used in the monitoring of therapies. In addition, these genes identify therapeutic targets, the modification of which may prevent MS development or progression. Genes were identified by determination of expression profiling. A large number of genes showing altered patterns of expression were identified, with the most discriminatory genes being those for: phosphatidylinositol transfer protein, inducible nitric oxide synthase, CIC-1 (CLCN1) muscle chloride channel protein, placental bikunin (AMBP), receptor kinase ligand LERK-3/Ephrin-A3, GATA-4, thymopoietin, transcription factor E2f-2, S-adenosylmethionine synthetase, carcinoembryonic antigen, the ret oncogene, a G protein-linked receptor (clone GPCR W), GTP- binding protein RALB, tyrosine kinase Syk, LERK-2/Ephrin-B1, ELK1 tyrosine kinase oncogene, transcription factor SL1, phospholipase C, gastricsin (progastricsin), and the D13S824E locus.

IT **391964-05-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes showing altered patterns of expression in multiple sclerosis and their diagnostic and therapeutic uses)

RN 391964-05-9 HCAPLUS
CN NFX1 (human cell line Raji clone NFX.1 cDNA #16) (9CI) (CA INDEX NAME)

SEQ
```
  1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
 51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
151 KPKKATQFVY SYARGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDPEKCT
301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLNCG
701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
751 ECTQTCARVH ECDHPVYHSG HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
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       851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
       901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
       951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
      1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
      1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
      1101 DVQD
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L20 ANSWER 10 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:837371 HCAPLUS
DN 139:333132
TI Targets for therapeutic intervention identified in the human mitochondrial proteome
IN Ghosh, Soumitra S.; Fahy, Eoin D.; Zhang, Bing; Gibson, Bradford W.; Taylor, Steven W.; Glenn, Gary M.; Warnock, Dale E.
PA Mitokor, USA; The Buck Institute for Age Research
SO PCT Int. Appl., 180 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2003087768	A2	20031023	2003WO-US10870	20030404 <--
WO2003087768	A3	20051124		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US2004101874	A1	20040527	2003US-0408765	20030404 <--
PRAI 2002US-372843P	P	20020412 <--		
2002US-389987P	P	20020617 <--		
2002US-412418P	P	20020920 <--		

AB Mitochondrial targets for drug screening assays and for therapeutic intervention in the treatment of diseases associated with altered mitochondrial function are provided. Complete amino acid sequences are provided for 3025 polypeptides that comprise the human heart mitochondrial proteome, using fractionated proteins derived from highly purified mitochondrial prepns., to identify previously unrecognized mitochondrial mol. components. Oxidative post-translational modification of tryptophan residues to N-formylkynurenine in cardiac mitochondrial proteins is also demonstrated by mass spectrometry.
IT **612115-69-2**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; targets for therapeutic intervention identified in the human mitochondrial proteome)
RN 612115-69-2 HCAPLUS
CN Protein (human heart clone GenBank gi:13242069 mitochondria-associated) (9CI) (CA INDEX NAME)

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SEQ      1 MAEAPPVSGT FKFNTDAAEF IPQEKKNSGL NCGTQRRLDS NRIGRRNYSS
        51 PPPCHLSRQV PYDEISAVHQ HSYHPSGSKP KSQQTSFQSS PCNKSPKSHG
       101 LQNQPWQKLR NEKHHIRVKK AQSLAEQTSD TAGLESSTRS ESGTDLREHS
       151 PSESEKEVVG ADPRGAKPKK ATQFVYSYGR GPKVKGKLKC EWSNRTTPKP
       201 EDAGPESTKP VGVFHPDSSE ASSRKGVLDG YGARRNEQRR YPQKRPPWEV
       251 EGARPRPGRN PPKQEGHRHT NAGHRNNMGP IPKDDLNERP AKSTCDSENL
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 301 AVINKSSRRV DQEKCTVRRQ DPQVVSPFSR GKQNHVLKNV ETHTGSLIEQ
 351 LTTEKYECMV CCELVRVTAP VWSCQSCYHV FHLNCIKKWA RSPASQADGQ
 401 SGWRCPACQN VSAHVPNTYT CFCGKVKNPE WSRNEIPHSC GEVCRKKQPG
 451 QDCPHSCNLL CHPGPCPPCP AFMTKTCECG RTRHTVRCGQ AVSVHCSNPC
 501 ENILNCGQHQ CAELCHGGQC QPCQIILNQV CYCGSTSRDV LCGTDVGKSD
 551 GFGDFSCLKI CGKDLKCGNH TCSQVCHPQP CQQCPRLPQL VRCCPCGQTP
 601 LSQLLELGSS SRKTCMDPVP SCGKVCGKPL PCGSLDFIHT CEKLCHEGDC
 651 GPCSRTSVIS CRCSFRTKEL PCTSLKSEDA TFMCDKRCNK KRLCGRHKCN
 701 EICCVDKEHK CPLICGRKLR CGLHRCEEPC HRGNCQTCWQ ASFDELTCHC
 751 GASVIYPPVP CGTRPPECTQ TCARVHECDH PVYHSCHSEE KCPPCTFLTQ
 801 KWCMGKHEFR SNIPCHLVDI SCGLPCSATL PCGMHKCQRL CHKGECLVDE
 851 PCKQPCTTPR ADCGHPCMAP CHTSSPCPVT ACKAKVELQC ECGRRKEMVI
 901 CSEASSTYQR IAAISMASKI TDMQLGGSVE ISKLITKKEV HQARLECDEE
 951 CSALERKKRL AEAFHISEDS DPFNIRSSGS KFSDSLKEDA RKDLKFVSDV
1001 EKEMETLVEA VNKVEVETSH WTFL
```

L20 ANSWER 11 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:697219 HCAPLUS
DN 139:192570
TI Nucleic acid and encoded amino acid sequences relating to Klebsiella pneumoniae for diagnostics and therapeutics
IN Breton, Gary L.; Osborne, Mark
PA Genome Therapeutics Corporation, USA
SO U.S., 932 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US---6610836	B1	20030826	2000US-0489039	20000127 <--
PRAI	1999US-117747P	P	19990129 <--		

AB The invention provides 7171 isolated polypeptide and 7171 genomic nucleic acid sequences derived from Klebsiella pneumoniae strain 93,19097 (ATCC 202080) that are useful in diagnosis and therapy of pathol. conditions. The nucleotide sequences include those of two naturally occurring plasmids in K. pneumoniae. Antibodies against the polypeptides, and methods for the production of recombinant polypeptides are also provided. The invention also provides methods for the detection, prevention, and treatment of pathol. conditions resulting from bacterial infection. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **581882-37-3**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acid and encoded amino acid sequences relating to Klebsiella pneumoniae for diagnostics and therapeutics)
RN 581882-37-3 HCAPLUS
CN Protein (Klebsiella pneumoniae strain ATCC202080 clone US6610836-SEQID-8731 open reading frame-encoded) (9CI) (CA INDEX NAME)

```
SEQ   1 MSLAPRKPGF YIPLRKHISP DCKRDILFRR GTQIQAGDSL GAACYKRLIP
     51 AAKAKAVNHT RDIPQTFWRD DRLPWLELRS TWRSRQAYKR HSHPQLSVGA
    101 IIEGETRCLC AGQEYLLQPG DLIVIPPHAP HSCNPLHGRP RSYHMLYLDA
    151 TWCHAQRPDI PPGASITSPQ PLLRDSPLFA SFQQVVALMS RGSLEQLPAR
    201 LAQLLHALPL CAAAPQAPHH ASALLFQCLA MDLPASPSLD KLAHDSALRK
    251 ETVIRAVKQD TGLTPASLIN MARIEYAKTR LRAGDPIADV GYQAGFADQS
    301 HFHKTFVSYT AATPRQYAQS RSISDNK
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L20 ANSWER 12 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:511464 HCAPLUS
DN 139:64457
TI Nucleic acids and their encoded polypeptides from human tissues
IN Tang, Y. Tom; Asundi, Vinod; Goodrich, Ryle W.; Ren, Feiyan; Zhang,.Jie; Zhao, Qing A.; Wang, Jian-rui; Ghosh, Malabika; Xue, Aidong J.; Wehrman, Tom; Weng, Gezhi; Zhou, Ping; Drmanac, Radoje T.; Wang, Zhiwei; Ma, Yunqing; Wang, Dunrui; Chen, Rui-hong; Xu, Chongjun; Boyle, Bryan J.
PA Hyseq, Inc., USA; et al.
SO PCT Int. Appl., 1177 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 123

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO2003054152	A2	20030703	2002WO-US39555	20021210 <--
	WO2003054152	A3	20041216		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US2004219521	A1	20041104	2002US-0128558	20020422 <--
	CA---2469941	AA	20030703	2002CA-2469941	20021210 <--
	EP---1504099	A2	20050209	2002EP-0805571	20021210 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
PRAI	2001US-339739P	P	20011210 <--		
	2001US-339453P	P	20011211 <--		
	2002US-365091P	P	20020314 <--		
	2002US-365384P	P	20020314 <--		
	2002US-372381P	P	20020412 <--		
	2002US-372615P	P	20020412 <--		
	2002US-0128558	A2	20020422 <--		
	2002US-376045P	P	20020424 <--		
	2000US-0488725	A2	20000121 <--		
	2000US-0491404	B2	20000125 <--		
	2000US-0552317	B2	20000425 <--		
	2000WO-US35017	A2	20001222 <--		
	2001WO-US02623	A2	20010125 <--		
	2001WO-US03800	A	20010205 <--		
	2001WO-US04927	A	20010226 <--		
	2001WO-US04941	A	20010305 <--		
	2001WO-US08631	A	20010330 <--		
	2001WO-US08656	A	20010416 <--		
	2002WO-US39555	W	20021210 <--		

AB The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof. Thus, 911 novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosomes using standard PCR, SBH (sequencing-by-hybridization) sequence signature anal., and Sanger sequencing techniques. Novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by the above methods, and in some cases sequences obtained from one or more public databases, using a recursive algorithm to extend the seed EST into an extended assemblage. Tissue expression profiles and nearest neighbor sequence homologies are provided. The sequences of this invention have applications in nucleic acid or polypeptide arrays, in the identification of binding mols., and in treatment of diseases.

IT 548553-97-5P
RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)
RN 548553-97-5 HCAPLUS
CN Protein (human clone WO03054152-SEQID-1231) (9CI) (CA INDEX NAME)

SEQ 1 MPVMSQLLSV HSEPSLLFLL TFPHSCNPPS LPSSSLSLSL THTHTHTHTH
51 STHTHISRVL Q

L20 ANSWER 13 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:409169 HCAPLUS
DN 138:380506
TI Genes that are differentially expressed during erythropoiesis and their diagnostic and therapeutic uses
IN Brissette, William H.; Neote, Kuldeep S.; Zagouras, Panayiotis; Zenke, Martin; Lemke, Britt; Hacker, Christine
PA Pfizer Products Inc., USA; Max-Delbrueck-Centrum Fuer Molekulare Medizin
SO PCT Int. Appl., 285 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2003038130	A2	20030508	2002WO-XA34888	20021031 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO2003038130	A2	20030508	2002WO-US34888	20021031 <--
WO2003038130	A3	20040212		
WO2003038130	C1	20040422		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
PRAI 2001US-335048P	P	20011031 <--		
2001US-335183P	P	20011102 <--		
2002WO-US34888	A	20021031 <--		

AB The present invention provides mol. targets that regulate erythropoiesis. Groups of genes or their encoded gene products comprise panels of the invention and may be used in therapeutic intervention, therapeutic agent screening, and in diagnostic methods for diseases and/or disorders of erythropoiesis. The panels were discovered using gene expression profiling of erythroid progenitors with Affymetrix HU6800 and HG-U95Av2

chips. Cells from an in vitro growth and differentiation system of SCF-Epo dependent human erythroid progenitors, E-cadherin+/CD36+ progenitors, cord blood, or CD34+ peripheral blood stem cells were analyzed. The HU6800 chip contains probes from 13,000 genes with a potential role in cell growth, proliferation, and differentiation and the HG-U95Av2 chip contains 12,000 full-length, functionally-characterized genes. [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 391964-05-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes that are differentially expressed during erythropoiesis and their diagnostic and therapeutic uses)

RN 391964-05-9 HCAPLUS

CN NFX1 (human cell line Raji clone NFX.1 cDNA #16) (9CI) (CA INDEX NAME)

SEQ

```
    1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
   51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
  101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
  151 KPKKATQFVY SYARGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
  201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
  251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDPEKCT
  301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
  351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
  401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
  451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
  501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
  551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
  601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
  651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLNCG
  701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
  751 ECTQTCARVH ECDHPVYHSG HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
  801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
  851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
  901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
  951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
 1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
 1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
 1101 DVQD
```

L20 ANSWER 14 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:381677 HCAPLUS

DN 138:349762

TI Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics

IN Breton, Gary; Bush, David

PA Genome Therapeutics Corporation, USA

SO U.S., 328 pp.
CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US---6562958	B1	20030513	1999US-0328352	19990604 <--
	US---6562958	B1	20030513	1999US-0328352	19990604 <--
PRAI	1998US-088701P	P	19980609 <--		
	1999US-0328352	A	19990604 <--		

AB The invention provides 4126 nucleic acid sequences derived from a genomic library of Acinetobacter baumannii strain 15839, as well as the derived open reading frames and protein-coding sequences. These sequences are

useful in diagnosis and therapy of pathol. conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathol. conditions resulting from bacterial infection. [This abstract record is one of 2 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 518375-13-8
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics)

RN 518375-13-8 HCAPLUS

CN Protein (Acinetobacter baumannii strain 15839 clone US6562958-SEQID-4825 open reading frame-encoded) (9CI) (CA INDEX NAME)

SEQ 1 VDLYPDRIIA VLDSMGVICA LGDLPHSCNH VAGIHLYDAY HRLLEHGKRK
51 TLMVLPNCQT MVGLNFFNLI W

L20 ANSWER 15 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:282587 HCAPLUS

DN 138:266971

TI Nucleic acids and their encoded polypeptides from human tissues

IN Tang, Tom Y.; Zhang, Jie; Ren, Feiyan; Xue, Aidong J.; Zhao, Qing A.; Wang, Jian-rui; Wehrman, Tom; Zhou, Ping; Ghosh, Malabika; Wang, Dunrui; Ma, Yunqing; Asundi, Vinod; Wang, Zhiwei; Weng, Gezhi; Haley-Vicente, Dana; Drmanac, Rodoje T.

PA Hyseq, Inc., USA

SO PCT Int. Appl., 1185 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2003029271	A2	20030410	2002WO-US30474	20020924 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA---2461280	AA	20030410	2002CA-2461280	20020924 <--
EP---1430112	A2	20040623	2002EP-0780359	20020924 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
PRAI 2001US-324631P	P	20010924 <--		
2002WO-US30474	W	20020924 <--		

AB The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof. Thus, 971 novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosomes using standard PCR, SBH (sequencing-by-hybridization) sequence signature anal., and Sanger sequencing techniques. Novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by the above methods, and in some cases sequences obtained from one or more public databases, using a recursive algorithm to extend the seed EST into an extended assemblage. Tissue expression profiles and

nearest neighbor sequence homologies are provided. The sequences of this invention have applications in nucleic acid or polypeptide arrays, in the identification of binding mols., and in treatment of diseases. The present invention claims a total of 6180 cDNA sequences, and discusses an addnl. 6180 encoded polypeptide sequences, but the Sequence Listing was not made available on publication of the patent application.

IT **503262-18-8P**
RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

RN 503262-18-8 HCAPLUS

CN Protein (human clone WO03029271-SEQID-3115 contig) (9CI) (CA INDEX NAME)

SEQ
```
  1 MEEVDHESKD VSGLWNLQRK VHIREKPYGC NEHGKVFRVS SSLTNRQVIH
 51 IADKTYKCSD CGEIFSSNSN FAQHQRIHTG EKPYKYNECG KVFNQNSHLA
101 QHQKIHTGQK PYNNKECGKV FSHHAYLAQH RKIHTGEKPY KCSECGKAFS
151 VCSSLTAHLV IHTGEKPYDC KECGKVFRHK SSLTTHQTVH TGERPYKCNE
201 CGKGFSRIAF LARHRKVHTG EKPYKCNECG KVFIGNSRLA RHRKIHTGGR
251 RYKCNECGKA FRTCSDLTAH LLIHTGEKPY ECIDCGKVFR HKSSLTYHCR
301 IHTGEKPYKC NECGKVFSQN SNLQRHRKIH TGEKLYKCNE CGKVFRQNSH
351 LAQHRDIHTG EKPYSCNECG KVFRRNSHLV RHRNVHTGEK PYSCNECGKV
401 FSRNSHLARH RNIHTGEKPH SCNECGKVFS RNSHLARHRK IHTGEKLYKC
451 NECSKVFSRN SRLAQHRNIH TGVKPYSCNE CGKVFSKNSI LVQHCSIHTR
501 EKP
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L20 ANSWER 16 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:55959 HCAPLUS

DN 138:84325

TI Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

AU Strausberg, Robert L.; Feingold, Elise A.; Grouse, Lynette H.; Derge, Jeffery G.; Klausner, Richard D.; Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn M.; Schuler, Gregory D.; Altschul, Stephen F.; Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather; Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh, Florence; Diatchenko, Luda; Marusina, Kate; Farmer, Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton, Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant, Tom L.; Scheetz, Todd E.; Brownstein, Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero; Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.; Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan, Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.; Richards, Stephen; Worley, Kim C.; Hale, Sarah; Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.; Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica; Helton, Erin; Ketteman, Mark; Madan, Anuradha; Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle; Madan, Anup; Young, Alice C.; Shevchenko, Yuriy; Bouffard, Gerard G.; Blakesley, Robert W.; Touchman, Jeffrey W.; Green, Eric D.; Dickson, Mark C.; Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy; Myers, Richard M.; Butterfield, Yaron S. N.; Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones, Steven J. M.; Marra, Marco A.

CS National Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA

SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

AB The National Institutes of Health Mammalian Gene Collection (MGC) Program

is a multiinstitutional effort to identify and sequence a cDNA clone containing a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstract record is one of eleven records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **479888-56-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)

RN 479888-56-7 HCAPLUS

CN Protein FLJ14299 (human clone MGC:44951 IMAGE:5527569) (9CI) (CA INDEX NAME)

SEQ
```
  1 MSDSPAGSNP RTPESSGSGS GGGGKRPAVP AAVSLLPPAD PLRQANRLPI
 51 RVLKMLSAHT GHLLHPEYLQ PLSSTPVSPI ELDAKKSPLA LLAQTCSQIG
101 KPDPPPSSKL NSVAAAANGL GAEKDPGRSA PGAASAAAAL KQLGDSPAED
151 KSSFKPYSKG SGGGDSRKDS GSSSVSSTSS SSSSSPGDKA GFRVPSAACP
201 PFPPHGAPVS ASSSSSSPGG SRGGSPHHSD CKNGGGVGGG ELDKKDQEPK
251 PSPEPAAVSR GGGGEPGAHG GAESGASGRK SEPPSALVGA GHVAPVSPYK
301 PGHSVFPLPP SSIGYHGSIV GAYAGYPSQF VPGLDPSKSG LVGGQLSGGL
351 GLPPGKPPSS SPLTGASPPS FLQGLCRDPY CLGGYHGASH LGGSSCSTCS
401 AHDPAGPSLK AGGYPLVYPG HPLQPAALSS SAAQAALPGH PLYTYGFMLQ
451 NEPLPHSCNW VAASGPCDKR FATSEELLSH LRTHTALPGA EKLLAAYPGA
501 SGLGSAAAAA AAAASCHLHL PPPAAPGSPG SLSLRNPHTL GLSRYHPYGK
551 SHLSTAGGLA VPSLPTAGPY YSPYALYGQR LASASALGYQ
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L20 ANSWER 17 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:55946 HCAPLUS

DN 138:84320

TI Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

AU Strausberg, Robert L.; Feingold, Elise A.; Grouse, Lynette H.; Derge, Jeffery G.; Klausner, Richard D.; Collins, Francis S.; Wagner, Lukas; Shenmen, Carolyn M.; Schuler, Gregory D.; Altschul, Stephen F.; Zeeberg, Barry; Buetow, Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.; Hopkins, Ralph F.; Jordan, Heather; Moore, Troy; Max, Steve I.; Wang, Jun; Hsieh, Florence; Diatchenko, Luda; Marusina, Kate; Farmer, Andrew A.; Rubin, Gerald M.; Hong, Ling; Stapleton, Mark; Soares, M. Bento; Bonaldo, Maria F.; Casavant, Tom L.; Scheetz, Todd E.; Brownstein, Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki; Carninci, Piero; Prange, Christa; Raha, Sam S.; Loquellano, Naomi A.; Peters, Garrick J.; Abramson, Rick D.; Mullahy, Sara J.; Bosak, Stephanie A.; McEwan, Paul J.; McKernan, Kevin J.; Malek, Joel A.; Gunaratne, Preethi H.; Richards, Stephen; Worley, Kim C.; Hale, Sarah; Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen W.; Villalon, Debbie K.; Muzny, Donna M.; Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard A.; Fahey, Jessica; Helton, Erin; Ketteman, Mark; Madan, Anuradha; Rodrigues, Stephanie; Sanchez, Amy; Whiting, Michelle; Madan, Anup; Young, Alice C.; Shevchenko, Yuriy; Bouffard, Gerard G.; Blakesley, Robert W.; Touchman, Jeffrey W.; Green, Eric D.; Dickson, Mark C.; Rodriguez, Alex C.; Grimwood, Jane; Schmutz, Jeremy; Myers, Richard M.; Butterfield, Yaron S. N.; Krzywinski, Martin I.; Skalska, Ursula; Smailus, Duane E.; Schnerch, Angelique; Schein, Jacqueline E.; Jones, Steven J. M.; Marra, Marco A.

CS Mammalian Gene Collection (MGC) Program Team, National Cancer Institute, NIH, Bethesda, MD, 20892-2580, USA

SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(26), 16899-16903
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The National Institutes of Health Mammalian Gene Collection (MGC) Program is a multiinstitutional effort to identify and sequence a cDNA clone containing a complete ORF for each human and mouse gene. ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstract record is one of eleven records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT 480793-91-7
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)
RN 480793-91-7 HCAPLUS
CN Protein (human clone MGC:20369 IMAGE:4558442) (9CI) (CA INDEX NAME)

SEQ
```
   1 MAEAPPVSGT FKFNTDAAEF IPQEKKNSGL NCGTQRRLDS NRIGRRNYSS
  51 PPPCHLSRQV PYDEISAVHQ HSYHPSGSKP KSQQTSFQSS PCNKSPKSHG
 101 LQNQPWQKLR NEKHHIRVKK AQSLAEQTSD TAGLESSTRS ESGTDLREHS
 151 PSESEKEVVG ADPRGAKPKK ATQFVYSYGR GPKVKGKLKC EWSNRTTPKP
 201 EDAGPESTKP VGVFHPDSSE ASSRKGVLDG YGARRNEQRR YPQKRPPWEV
 251 EGARPRPGRN PPKQEGHRHT NAGHRNNMGP IPKDDLNERP AKSTCDSENL
 301 AVINKSSRRV DQEKCTVRRQ DPQVVSPFSR GKQNHVLKNV ETHTGSLIEQ
 351 LTTEKYECMV CCELVRVTAP VWSCQSCYHV FHLNCIKKWA RSPASQADGQ
 401 SGWRCPACQN VSAHVPNTYT CFCGKVKNPE WSRNEIPHSC GEVCRKKQPG
 451 QDCPHSCNLL CHPGPCPPCP AFMTKTCECG RTRHTVRCGQ AVSVHCSNPC
 501 ENILNCGQHQ CAELCHGGQC QPCQIILNQV CYCGSTSRDV LCGTDVGKSD
 551 GFGDFSCLKI CGKDLKCGNH TCSQVCHPQP CQQCPRLPQL VRCCPCGQTP
 601 LSQLLELGSS SRKTCMDPVP SCGKVCGKPL PCGSLDFIHT CEKLCHEGDC
 651 GPCSRTSVIS CRCSFRTKEL PCTSLKSEDA TFMCDKRCNK KRLCGRHKCN
 701 EICCVDKEHK CPLICGRKLR CGLHRCEEPC HRGNCQTCWQ ASFDELTCHC
 751 GASVIYPPVP CGTRPPECTQ TCARVHECDH PVYHSCHSEE KCPPCTFLTQ
 801 KWCMGKHEFR SNIPCHLVDI SCGLPCSATL PCGMHKCQRL CHKGECLVDE
 851 PCKQPCTTPR ADCGHPCMAP CHTSSPCPVT ACKAKVELQC ECGRRKEMVI
 901 CSEASSTYQR IAAISMASKI TDMQLGGSVE ISKLITKKEV HQARLECDEE
 951 CSALERKKRL AEAFHISEDS DPFNIRSSGS KFSDSLKEDA RKDLKFVSDV
1001 EKEMETLVEA VNKGKNSKKS HSFPPMNRDH RRIIHDLAQV YGLESVSYDS
1051 EPKRNVVVTA IRGKSVCPPT TLTGVLEREM QARPPPPIPH HRHQSDKNPG
1101 SSNLQKITKE PIIDYFDVQD
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L20 ANSWER 18 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:6504 HCAPLUS
DN 138:164516
TI Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AU Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins,

S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CS Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

SO Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstract record is one of thirty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **493548-19-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

RN 493548-19-9 HCAPLUS

CN Protein (mouse strain C57BL/6J clone 9330101C04 818-amino acid) (9CI) (CA INDEX NAME)

SEQ
```
  1 MAEAPPVSGT FKFNTDAAEF IPQERKTSGL NCGTQRRLDS SRIGRRNYNS
 51 SPPCHLPRHI PYEDISAVHQ HSYASGSKPK SPQGFFQSSN KSLKNHGLQN
101 QPWQKARNEK HQNRNKKAQG LSEQTSDTSS LESVARSESG TNPREHSPSE
151 SEKEVVIADP RGAKPKKAAQ LTYNYGRGPK AKGRLRSEWG NRMSPKSEDE
201 NTRPVAISHT DSSDASCRKP VVDPCVCRRN EQRRYPQKRP PWEVEGARPR
251 PGRNPPKQES QRHINAGPKT NMSPIPKDNL RERPTKSACD TGNLAVVSKS
301 SRRVNQEKTA VRRQDPQVLS PFPRGKQNHM LKNVETHTGS LIEQLTTEKY
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  351 ECMVCCELVQ VTAPVWSCQS CFHVFHLNCI KKWARSPASH ADGQSGWRCP
  401 ACQNVSAHVP NTYTCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS
  451 CNLLCHPGPC PPCPAFTTKT CECGRTRHTV RCGQPVSVHC SNACENILNC
  501 GQHHCAELCH GGQCQPCRII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS
  551 CLKICGKDLK CGSHTCSQVC HPQPCQPCPR LPHLVRYCPC GQTPLSQLLE
  601 HGSNARKTCM DPVPSCGKVC GKPLACGSSD FIHTCEKLCH EGDCGPCSRT
  651 SVISCRCSFR TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD
  701 KEHKCPLICG RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY
  751 PPVPCGTRPP ECTQTCARIH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK
  801 HEELTIKKLW TFKETLDF
```

L20 ANSWER 19 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:982555 HCAPLUS
DN 138:84297
TI Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AU Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.
CS Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
SO Nature (London, United Kingdom) (2002), 420(6915), 563-573
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs.

The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstract record is one of thirty records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 326053-89-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

RN 326053-89-8 HCAPLUS

CN Protein (mouse strain C57BL/6J clone 1300017N15 818-amino acid) (9CI) (CA INDEX NAME)

SEQ
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  1 MAEAPPVSGT FKFNTDAAEF IPQERKTSGL NCGTQRRLDS SRIGRRNYSS
 51 SPPCHLPRHI PYEDISAVHQ HSYASGSKPK SPQGFFQSSN KSLKNHGLQN
101 QPWQKARNEK HQNRNKKAQG LSEQTSDTSS LESVARSESG TNPREHSPSE
151 SEKEVVIADP RGAKPKKAAQ LTYNYGRGPK AKGRLRSEWG NRMSPKSEDE
201 NTRPVAISHT DSSDASCRKP VVDPCVCRRN EQRRYPQKRP PWEVEGARPR
251 PGRNPPKQES QRHINAGPKT NMSPIPKDNL RERPTKSACD TGNLAVVSKS
301 SRRVNQEKTA VRRQDPQVLS PFPRGKQNHM LKNVETHTGS LIEQLTTEKY
351 ECMVCCELVQ VTAPVWSCQS CFHVFHLNCI KKWARSPASH ADGQSGWRCP
401 ACQNVSAHVP NTYTCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS
451 CNLLCHPGPC PPCPAFTTKT CECGRTRHTV RCGQPVSVHC SNACENILNC
501 GQHHCAELCH GGQCQPCRII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS
551 CLKICGKDLK CGSHTCSQVC HPQPCQPCPR LPHLVRYCPC GQTPLSQLLE
601 HGSNARKTCM DPVPSCGKVC GKPLACGSSD FIHTCEKLCH EGDCGPCSRT
651 SVISCRCSFR TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD
701 KEHKCPLICG RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY
751 PPVPCGTRPP ECTQTCARIH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK
801 HEELTIKKLW TFKETLDF
```

L20 ANSWER 20 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2002:752116 HCAPLUS

DN 137:289735

TI Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13

AU Hall, N.; Pain, A.; Berriman, M.; Churcher, C.; Harris, B.; Harris, D.; Mungall, K.; Bowman, S.; Atkin, R.; Baker, S.; Barron, A.; Brooks, K.; Buckee, C. O.; Burrows, C.; Cherevach, I.; Chillingworth, C.; Chillingworth, T.; Christodoulou, Z.; Clark, L.; Clark, R.; Corton, C.; Cronin, A.; Davies, R.; Davis, P.; Dear, P.; Dearden, F.; Doggett, J.; Feltwell, T.; Goble, A.; Goodhead, I.; Gwilliam, R.; Hamlin, N.; Hance, Z.; Harper, D.; Hauser, H.; Hornsby, T.; Holroyd, S.; Horrocks, P.; Humphray, S.; Jagels, K.; James, K. D.; Johnson, D.; Kerhornou, A.; Knights, A.; Konfortov, B.; Kyes, S.; Larke, N.; Lawson, D.; Lennard, N.; Line, A.; Maddison, M.; McLean, J.; Mooney, P.; Moule, S.; Murphy, L.; Oliver, K.; Ormond, D.; Price, C.; Quail, M. A.; Rabbinowitsch, E.; Rajandream, M.-A.; Rutter, S.; Rutherford, K. M.; Sanders, M.; Simmonds, M.; Seeger, K.; Sharp, S.; Smith, R.; Squares, R.; Squares, S.; Stevens, K.; Taylor, K.; Tivey, A.; Unwin, L.; Whitehead, S.; Woodward, J.; Sulston, J. E.; Craig, A.; Newbold, C.; Barrell, B. G.

CS The Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA, UK

SO Nature (London, United Kingdom) (2002), 419(6906), 527-531
CODEN: NATUAS; ISSN: 0028-0836

PB Nature Publishing Group

DT Journal

LA English

AB Since the sequencing of the first two chromosomes of the malaria parasite, Plasmodium falciparum, there has been a concerted effort to sequence and

assemble the entire genome of this organism. This report provides the sequence of chromosomes 1, 3-9 and 13 of P. falciparum clone 3D7; these chromosomes account for .apprx.55% of the total genome. The methods used to map, sequence and annotate these chromosomes is described. By comparing these assemblies with the optical map, the completeness of the resulting sequence is indicated. During annotation, Gene Ontol. terms were assigned to the predicted gene products, and clustering of some malaria-specific terms to specific chromosomes was observed A highly conserved sequence element was found in the intergenic region of internal var genes that is not associated with their telomeric counterparts.

IT 467533-29-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13)

RN 467533-29-5 HCAPLUS

CN Protein (Plasmodium falciparum strain 3D7 gene PFI1410c) (9CI) (CA INDEX NAME)

SEQ
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   1 MNLHSAIYPL YKLVITKPTH KKKSVPLYWV ALKSTSINNV EGNIKKCKRW
  51 NEECYKLKKK VPSKNEDDID IDKLNYMIRK ERERKKKNKI KEKDNNNDNN
 101 NDDNNNDNNN DNNNEEEEKK NYKKEGYFKY HDYDYDYHRD DVMKASIHMN
 151 KKENIWNMFN LDNKGYIKNV NIKINDTHLM DECINYCNTW NIQKICYKNV
 201 ANNNIHIIEK LETTPLERNN IINDKMDNIN NQANKMNSTY NNNNYNNNNS
 251 CYNYNEIKTF DHQEKNIHTP TNTNDIYDIN NYYDILENEH SLEIMKKKNS
 301 YNKLFDENDA RLKWDTQYDT YYSNDDIKYF NQYNDHNYWN YIYTLDLNKN
 351 VYLNDLGRNK PIQFLNKFQI LQILYENIDK VLETDNLNMC YNTDNIKIYD
 401 NFQKNKICVR NFTNFDSVKN QKDLIHPHHQ GNNLKELDKG EKKKKNSVHY
 451 FEEEILLKYI INFKYDKNKE INEIENPNKK HDNVNFFYHI LNRIEFISVS
 501 FNLRESIFIL CFFYLYNFLS FEILNKFIQN ILLHIHDLNI VQTLILLNIY
 551 GTFKSNYEDV IHLLLMYFYN IQGTHLSKYN LKENKITKKQ NKNDHKFVTY
 601 YNHDESICTH DIPMKDNTYN VTYDMIFLNI CLQYNIHINN SLMLFFTKYH
 651 IHFYKNKIDS SLIPFQCFCF LTDGKNEHLF FKTLQSFSSL LNTHIVQQTS
 701 PGLRHILKNL QQNITTPRFT IEQLSKIISA LNFLDIEKWI RHMFTYIKRY
 751 NYMGLPKVGD HIKICDDIKT YDGIKTYDDI KTYDGIKTYD HIKTYDGIKT
 801 YDGIKTYDDI KTYDDIKTYD DIKTHDDIKT HDEITKRTTF EPPHSCNHKE
 851 QIFKSEHKLK PTYKEETKQN QPFNKHIINA NMKVINFLFF FNIVKNINRY
 901 FLFPFYDKYD LYELLKDEVF PEYKIKYQDG DITFSCLVHT DYKLVNQYED
 951 VKLFYKKDVD NDICHMPYNV ENDQVYSYGE YHKTNETDCL INLTKDDVKN
1001 LFIDNNNKLN TFLYNYKKIN IQNIPLKFIV DIIYFINKYG QMIIPFKNNI
1051 NIKENDDINE YILRILSFCY LKIYVLLNSY NNISKEKKYI LSHLYKIINN
1101 SYYLNNDILN YIPTSLSTLH KDMHMICSKK HFNLLSYFIL NLTKNLLPKT
1151 KNLYSSYHQN VINSYVQNIN INTNINTNTN TNINTINKNY YKLTYSIYKT
1201 LLSIYYNFFD YIKESFDILI FLKNSKNIFF SLCIYLYNIA KIMMLKHPYD
1251 MTLQYYLSSL YNINIKINNN GNINNNDNNN DLYIPLEIYK LILNLLKKCI
1301 SFFYLHKDNI IQHIVSNDDV IDFLNTLSYF NISLYYYKYL LNIIQTNDTM
1351 PQEKKTSDRN HINNTYNTVM STYEEETTCT YYQQYHDNIF SYFFKHLIQI
1401 KTNCINDLNE SNKLILFKTL TKLFVFNKYK NVLHMDHITI LLNQIMHFVI
1451 IHHMYISKHN YFFIISSYIN LKKNYDIVKQ DKTFNHTAYQ KLAHICEQII
1501 I
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RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Adhya, S	1989	23	227	Annu Rev Genet	HCAPLUS
Apweiler, R	2001	29	37	Nucleic Acids Res	HCAPLUS
Ashburner, M	2000	25	25	Nature Genet	HCAPLUS
Bateman, A	2002	30	276	Nucleic Acids Res	HCAPLUS
Berriman, M	2001	17	463	Trends Parasitol	MEDLINE
Bowman, S	1999	400	532	Nature	HCAPLUS
Cawley, S	2001	118	167	Mol Biochem Parasito	HCAPLUS
Claros, M	1996	241	779	Eur J Biochem	HCAPLUS

de Bruin, D	1992	14	332	Genomics	HCAPLUS
Deitsch, K	2001	412	875	Nature	HCAPLUS
Emanuelsson, O	2000	300	1005	J Mol Biol	HCAPLUS
Figueiredo, L	2002	21	815	EMBO J	HCAPLUS
Florens, L	2002	419	520	Nature	HCAPLUS
Gardner, M	1998	282	1126	Science	HCAPLUS
Glockner, G	2002	418	79	Nature	
Hapgood, J	2001	25	17	Cell Biol Int	HCAPLUS
Hyman, R	2002	419	534	Nature	HCAPLUS
Katinka, M	2001	414	450	Nature	HCAPLUS
Konfortov, B	2000	10	1737	Genome Res	HCAPLUS
Krogh, A	2001	305	567	J Mol Biol	HCAPLUS
Lai, Z	1999	23	309	Nature Genet	HCAPLUS
Lasonder, E	2002	419	531	Nature	
Nielsen, H	1999	12	3	Protein Eng	HCAPLUS
O'Donnell, R	2002	21	1231	EMBO J	HCAPLUS
Pachebat, J	2001	117	83	Mol Biochem Parasito	HCAPLUS
Piper, M	1998	8	1299	Genome Res	HCAPLUS
Quail, M	2001	12	355	DNA Seq	HCAPLUS
Rutherford, K	2000	16	944	Bioinformatics	HCAPLUS
Salzberg, S	1999	59	24	Genomics	HCAPLUS
Sonnhammer, E	1998	6	175	Proc Int Conf Intell	MEDLINE
Su, X	1999	286	1351	Science	HCAPLUS
Vazquez-Macias, A	2002	45	155	Mol Microbiol	HCAPLUS
Zdobnov, E	2001	17	847	Bioinformatics	HCAPLUS

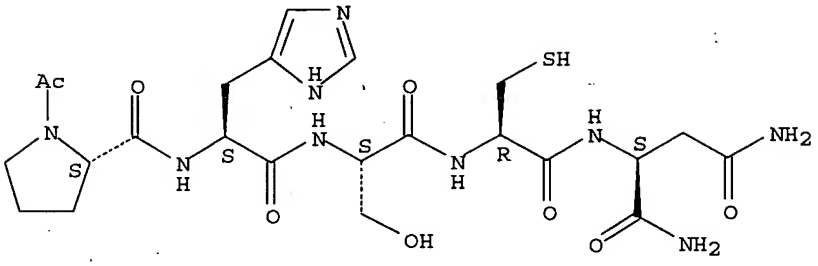
L20 ANSWER 21 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:631705 HCAPLUS
DN 138:297158
TI Suppression of Tumor Recurrence and Metastasis by a Combination of the PHSCN Sequence and the Antiangiogenic Compound Tetrathiomolybdate in Prostate Carcinoma
AU van Golen, Kenneth L.; Bao, Liwei; Brewer, George J.; Pienta, Kenneth J.; Kamradt, Jeffrey M.; Livant, Donna L.; Merajver, Sofia D.
CS Division of Hematology and Oncology, Department of Internal Medicine, University of Michigan Comprehensive Cancer Center, Ann Arbor, MI, 48109-0948, USA
SO Neoplasia (New York, NY, United States) (2002), 4(5), 373-379
CODEN: NEOPFL; ISSN: 1522-8002
PB Nature Publishing Group
DT Journal
LA English
AB Plasma fibronectin-mediated invasion of human DU145 prostate cancer cell line was efficaciously inhibited in a rat tumor model by treatment with Ac-PHSCN-NH2 peptide. Invasion of DU145 cells was stimulated by the PHSRN sequence of plasma fibronectin. However, PHSCN acts as a competitive inhibitor of PHSRN-mediated invasion. In the current study, we determined whether PHSCN could inhibit the recurrence and metastasis of DU145 tumors after excision of the primary tumor in an athymic nude mouse model. We demonstrated that mice treated thrice weekly with i.v. Ac-PHSCN-NH2 peptide survived tumor-free for more than 30 wk post-primary tumor excision, whereas their untreated counterparts succumbed to recurrence and/or metastatic disease in significantly less time. Because of the universal requirement for angiogenesis in solid tumor growth, we tested the efficacy of copper deficiency induced by tetrathiomolybdate (TM) to retard tumor growth in the Dunning prostate cancer model. Significant reduction in size of the primary tumor was observed in mice rendered copper deficient. We sought to reduce tumor growth at the primary and metastatic sites by combining the anti-invasion Ac-PHSCN-NH2 peptide with TM. Improved survival, fewer metastatic lesions, and excellent tolerability were observed with the combination therapy.
IT **262438-43-7**
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(suppression of tumor recurrence and metastasis by a combination of PHSCN sequence and the antiangiogenic compound tetrathiomolybdate in

prostate carcinoma)
RN 262438-43-7 HCAPLUS
CN L-Aspartamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

NTE modified

SEQ 1 PHSCN

Absolute stereochemistry.



RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Allen, M	1998	29	311	Hum Pathol	MEDLINE
American Cancer Society	2002			Cancer Facts and Fig	
Livant, D	1995	55	5085	Cancer Res	HCAPLUS
Livant, D	2000	60	309	Cancer Res	HCAPLUS
Mosher, D	1984	35	561	Annu Rev Med	HCAPLUS
Nozue, M	2001	8	1247	Oncol Rep	MEDLINE
Partin, A	2001	58	843	Urology	MEDLINE
Rokhlin, O	1995	26	205	Prostate	HCAPLUS
Romanov, V	1999	39	108	Prostate	HCAPLUS
Schroder, J	1998	45	1807	Hepatogastroenterolo	MEDLINE
Smith, D	1999	26	323	Urol Clin North Am	MEDLINE
Trikha, M	1996	56	5071	Cancer Res	HCAPLUS
Uchiyama, A	1999	81	721	Br J Cancer	MEDLINE
van Golen, K	1996	14	95	Clin Exp Metastasis	HCAPLUS
Webber, M	1995	1	1089	Clin Cancer Res	MEDLINE
Witkowski, C	1993	119	637	J Cancer Res Clin On	HCAPLUS
Zheng, D	1999	59	1655	Cancer Res	HCAPLUS

L20 ANSWER 22 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:555761 HCAPLUS
DN 137:121939
TI Compositions and methods for the use of fibronectin fragments in the diagnosis of cancer
IN Livant, Donna
PA The Regents of the University of Michigan, USA
SO PCT Int. Appl., 77 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2002057786	A2	20020725	2002WO-US01189	20020115 <--
WO2002057786	A3	20031211		

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PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
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KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB,
GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA,
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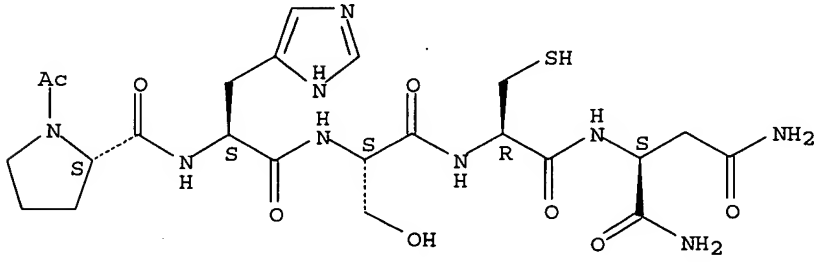
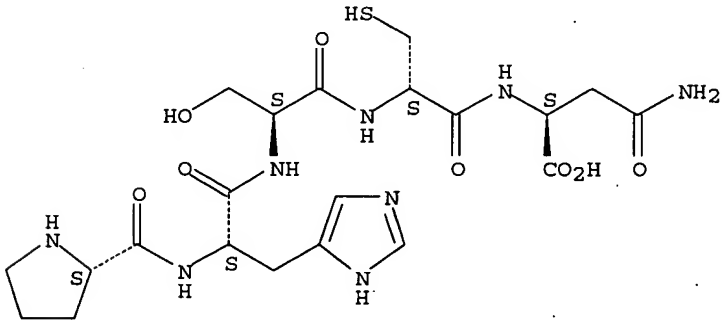
CA---2435320 AA 20020725 2002CA-2435320 20020115 <--
EP---1388013 A2 20040211 2002EP-0713418 20020115 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI 2001US-0765496 A 20010118 <--
2002WO-US01189 W 20020115 <--
OS MARPAT 137:121939
AB The present invention concerns the detection tumors in vivo, the imaging of tumors in vivo, and the imaging of cancerous tissue in pathol. samples. In particular the present invention incorporates the use of fibronectin fragments into these same detection and imaging methods.
IT **262438-43-7 443305-20-2 443305-23-5**
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(compns. and methods for use of fibronectin fragments in diagnosis of cancer)
RN 262438-43-7 HCAPLUS
CN L-Aspartamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



RN 443305-20-2 HCAPLUS
CN L-Asparagine, L-prolyl-L-histidyl-L-seryl-D-cysteinyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



RN 443305-23-5 HCAPLUS
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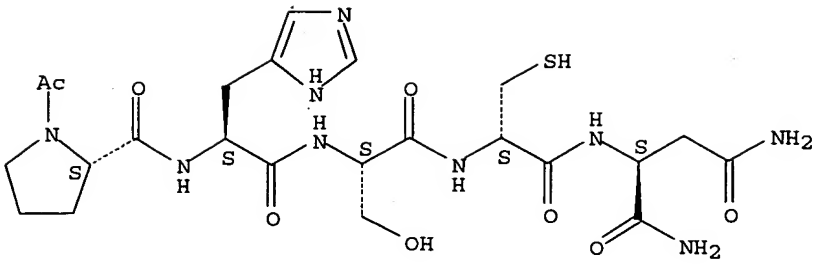
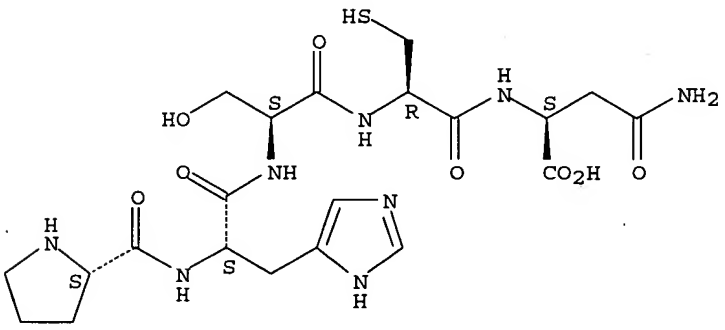
Absolute stereochemistry.



IT 252229-85-9P
RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(compns. and methods for use of fibronectin fragments in diagnosis of cancer)
RN 252229-85-9 HCAPLUS
CN L-Asparagine, L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

SEQ 1 PHSCN

Absolute stereochemistry.



L20 ANSWER 23 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:471209 HCAPLUS
DN 138:302256
TI Murine NFX.1: Isolation and characterization of its messenger RNA, mapping of its chromosomal location and assessment of its developmental expression
AU Arlotta, Paola; Miyazaki, Dai; Copeland, Neal G.; Gilbert, Debra J.; Jenkins, Nancy A.; Ono, Santa J.
CS The Schepens Eye Research Institute, Harvard Medical School, Boston, MA, USA
SO Immunology (2002), 106(2), 173-181
CODEN: IMMUAM; ISSN: 0019-2805
PB Blackwell Science Ltd.
DT Journal
LA English
AB The authors have previously isolated (by expression cloning) a human cDNA, termed NFX.1, encoding a nucleic acid-binding protein that interacts with the conserved X1 box cis-element first discovered in class II major histocompatibility complex (MHC) genes. Functional studies involving expression of NFX.1 and assessment of expression from class II reporter constructs and endogenous class II MHC genes indicated that the factor could repress transcription of class II MHC genes. Subsequent studies have extended the biol. significance of the factor, indicating that it

plays an important role in neuronal development. Indeed, the reiterated RING finger motifs in the central domain of the polypeptide strongly suggest that NF-X1 is a probable E3 ubiquitin protein ligase, indicating that the protein may have multiple activities. Here the authors report the cloning of the mouse homolog of the human NfX.1 cDNA: m-Nfx.1. Comparison of the deduced primary sequence of mouse and human NFX.1 proteins shows very high homol. and confirms that m-NFX.1 contains the conserved cysteine-rich DNA-binding motif first described in human NFX.1 (95% homol.). Expression of MHC class II genes is substantially reduced following expression of m-NFX.1, which confirms that the authors have isolated the functional murine homolog of human NfX.1 cDNA. Further evidence comes from the mapping of m-Nfx.1 gene to the proximal region of mouse chromosome 4, a region syntenic to the location of human Nfx.1 (short arm of chromosome 9). Expression profiling show that m-NFX.1 is expressed ubiquitously in both adult tissues and during development, supporting the hypothesis that it may have yet-undescribed roles in distinct biol. processes.

IT **484154-74-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence characterization, chromosomal mapping, and developmental expression for NFX.1 transcription factor of mouse)

RN 484154-74-7 HCAPLUS

CN Transcription factor NFX.1 (Mus musculus gene Nfx1) (9CI) (CA INDEX NAME)

SEQ
```
      1 MAEAPPVSGT FKFNTDAAEF IPQERKTSGL NCGTQRRLDS SRIGRRNYSS
     51 SPPCHLPRHI PYEDISAVHQ HSYASGSKPK SPQGFFQSSN KSLKNHGLQN
    101 QPWQKARNEK HQNRNKKAQG LSEQTSDTSS LESVARSESG TNPREHSPSE
    151 SEKEVVIADP RGAKPKKAAQ LTYNYGRGPK AKGRLRSEWG NRMSPKSEDE
    201 IPDPWRFPTL TLQIASCRKP VVDPCVCRRN EQRRYPQKRP PLGSGRARPR
    251 PGRNPPKQES QRHINAGPKT NMSPIPKDNL RERPTKSACD TGNLAVVSKS
    301 SRRVNQEKTA VRRQDPQVLS PFPRGKQNHM LKNVETHTGS LIEQLTTEKY
    351 ECMVCCELVQ VTAPVWSCQS CFHVFHLNCI KKWARSPASH ADGQSGWRCP
    401 ACQNVSAHVP NTYTCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS
    451 CNLLCHPGPC PPCPAFTTKT CECGRTRHTV RCGQPVSVHC SNACENILNC
    501 GQHHCAELCH GGQCQPCRII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS
    551 CLKICGKDLK CGSHTCSQVC HPQPCQPCPR LPHLVRYCPC GQTPLSQLLE
    601 HGSNARKTCM DPVPSCGKVC GKPLACGSSD FIHTCEKLCH EGDCGPCSRT
    651 SVISCRCSFR TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD
    701 KEHKCPLICG RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY
    751 PPVPCGTRPP ECTQTCARIH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK
    801 HELRSNIPCH LVDISCGLPC SAMLPCGMHK CQRLCHKGEC LVDEACKQPC
    851 TTPRGDCGHP CMAPCHPSLP CPVTACKAKV ELQCECGRRK EMVICSEASG
    901 TYQRIVAISM ASKITDMQLG DSVEISKLIT KKEVQQARLQ CDEECAALER
    951 RKRLAEAFDI TDDSDPFNVR SSASKFSDSL KDDARKDLKF VSDVEKEMET
   1001 LVEAVNKGKN NKKSHCFPPM NRDHRRIIHD LAQVYGLESI SYDSEPKRNV
   1051 VVTAVRGKSV CPPTTLTSVI ERETQTRPPP PIPHHRHQAD KAPGSSTLQK
   1101 IVKEAVIDYF DVQD
```

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Abdulkadir, S	1995	9	1429	FASEB J	HCAPLUS
Abdulkadir, S	1995	182	487	J Exp Med	MEDLINE
Benichou, B	1991	88	4285	Proc Natl Acad Sci U	HCAPLUS
Chapman, H	1998	10	93	Curr Opin Immunol	HCAPLUS
Copeland, N	1991	7	113	Trends Genet	HCAPLUS
Douhan, J	1996	8	255	Int Immunol	HCAPLUS
Durand, B	1994	14	6839	Mol Cell Biol	HCAPLUS
Glimcher, L	1992	10	13	Annu Rev Immunol	HCAPLUS
Harton, J	2000	20	6185	Mol Cell Biol	HCAPLUS
Harton, J	2000	20	6185	Mol Cell Biol	HCAPLUS

Hume, C	1989	26	288	Hum Immunol	HCAPLUS
Jenkins, N	1982	43	26	J Virol	HCAPLUS
King, D	1983	131	315	J Immunol	HCAPLUS
Lander, E	2001	409	860	Nature	HCAPLUS
Marbois, B	1994	15	83	Arch Biochem Biophys	
Masternak, K	1998	20	273	Nat Genet	HCAPLUS
Matsushima, G	1994	78	645	Cell	HCAPLUS
McDevitt, H	1998	10	677	Curr Opin Immunol	HCAPLUS
Morales, J	1999	96	14470	Proc Natl Acad Sci U	HCAPLUS
Song, Z	1994	180	1763	J Exp Med	HCAPLUS
Steimle, V	1993	75	135	Cell	HCAPLUS
Stroumbakis, N	1996	16	192	Mol Cell Biol	HCAPLUS
Tai, A	1999	36	447	Mol Immunol	HCAPLUS
Ting, J	1993	12	65	Immunol Res	HCAPLUS
Wert, S	1993	156	426	Dev Biol	HCAPLUS
Wright, K	1994	13	4042	EMBO J	HCAPLUS

L20 ANSWER 24 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:459968 HCAPLUS
DN 137:1525
TI Cloning, protein and cDNA sequence of human nuclear transcription factor-2 and their uses in therapy and diagnosis
IN Sha, Jiahao; Zhou, Zuomin; Li, Jianmin
PA Nanjing Medical Univ., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, *7 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI CN---1318556	A	20011024	2001CN-0113502	20010411 <--
PRAI 2001CN-0113502		20010411 <--		

AB The invention provides full-length cDNA sequence (3,613 bp) and ORF (open reading frame) sequence (3,075 bp, its coding 1024 amino acids) of one human nuclear transcription factor-2 (NFX2). The invention relates to preparation of fusion protein in which NFX2 is fused with GST. The invention also relates to preparation of monoclonal antibody and polyclonal antibody. The invention also relates to preparation of biochip for detecting mutations in gene NFX21 encoding nuclear transcription factor-2 and for drug screening. The invention further relates to application of fusion protein of NFX2 in treating NFX2-related diseases.

IT **432839-50-4P**
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning, protein and cDNA sequence of human nuclear transcription factor-2 and their uses in therapy and diagnosis)
RN 432839-50-4 HCAPLUS
CN Transcription factor NFX2 (nuclear transcription factor-2) (human) (9CI) (CA INDEX NAME)

SEQ
```
  1 MAEAPPVSGT FKFNTDAAEF IPQEKKNSGL NCGTQRRLDS NRIGRRNYSS
 51 PPPCHLSRQV PYDEISAVHQ HSYHPSGSKP KSQQTSFQSS PCNKSPKSHG
101 LQNQPWQKLR NEKHHIRVKK AQSLAEQTSD TAGLESSTRS ESGTDLREHS
151 PSESEKEVVG ADPRGAKPKK ATQFVYSYGR GPKVKGKLKC EWSNRTTPKP
201 EDAGPESTKP VGVFHPDSSE ASSRKGVLDG YGARRNEQRR YPQKRPPWEV
251 EGARPRPGRN PPKQEGHRHT NAGHRNNMGP IPKDDLNERP AKSTCDSENL
301 AVINKSSRRV DQEKCTVRRQ DPQVVSPFSR GKQNHVLKNV ETHTGSLIEQ
351 LTTEKYECMV CCELVRVTAP VWSCQSCYHV FHLNCIKKWA RSPASQADGQ
401 SGWRCPACQN VSAHVPNTYT CFCGKVKNPE WSRNEIPHSC GEVCRKKQPG
451 QDCPHSCNLL CHPGPCPPCP AFMTKTCECG RTRHTVRCGQ AVSVHCSNPC
501 ENILNCGQHQ CAELCHGGQC QPCQIILNQV CYCGSTSRDV LCGTDVGKSD
551 GFGDFSCLKI CGKDLKCGNH TCSQVCHPQP CQQCPRLPQL VRCCPCGQTP
601 LSQLLELGSS SRKTCMDPVP SCGKVCGKPL PCGSLDFIHT CEKLCHEGDC
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       651 GPCSRTSVIS CRCSFRTKEL PCTSLKSEDA TFMCDKRCNK KRLCGRHKCN
       701 EICCVDKEHK CPLICGRKLR CGLHRCEEPC HRGNCQTCWQ ASFDELTCHC
       751 GASVIYPPVP CGTRPPECTQ TCARVHECDH PVYHSCHSEE KCPPCTFLTQ
       801 KWCMGKHEFR SNIPCHLVDI SCGLPCSATL PCGMHKCQRL CHKGECLVDE
       851 PCKQPCTTPR ADCGHPCMAP CHTSSPCPVT ACKAKVELQC ECGRRKEMVI
       901 CSEASSTYQR IAAISMASKI TDMQLGGSVE ISKLITKKEV HQARLECDEE
       951 CSALERKKRL AEAFHISEDS DPFNIRSSGS KFSDSLKEDA RKDLKFVSDV
      1001 EKEMETLVEA VNKVEVETSH WTFL
```

L20 ANSWER 25 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:72748 HCAPLUS
DN 136:146104
TI Human stress genes identified using DNA microarrays
IN Chenchik, Alex; Lukashev, Matvey E.
PA Clontech Laboratories, Inc., USA
SO U.S. Pat. Appl. Publ., 57 pp., Cont.-in-part of U.S. Ser. No. 441,920.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US2002009730	A1	20020124	2001US-0782909	20010213 <--
PRAI 1998US-0222256	B2	19981228 <--		
1999US-0440305	B2	19991117 <--		
1999US-0441920	A2	19991117 <--		

AB Human stress arrays and methods for their use are provided. The subject arrays include a plurality of polynucleotide spots, each of which is made up of a polynucleotide probe composition of unique polynucleotides corresponding to a human stress gene. The average length of the polynucleotide probes is 50-1000 nucleotides. The d. of the spots on the array did not exceed 400/cm2 and the spots had a diameter ranging between 10 and 5000 μm. Furthermore, the number of polynucleotide probe spots on the array ranged between 50 and 2000 nucleotides. The subject arrays find use in hybridization assays, particularly in assays for the identification of differential gene expression of human stress genes. Two hundred thirty-six different human stress genes were identified using this approach.

IT **391964-05-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; human stress genes identified using DNA microarrays)
RN 391964-05-9 HCAPLUS
CN NFX1 (human cell line Raji clone NFX.1 cDNA #16) (9CI) (CA INDEX NAME)

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SEQ      1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
        51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
       101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
       151 KPKKATQFVY SYARGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
       201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
       251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDPEKCT
       301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
       351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
       401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
       451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
       501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
       551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
       601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
       651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLNCG
       701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
       751 ECTQTCARVH ECDHPVYHSG HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
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  801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
  851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
  901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
  951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
 1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
 1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
 1101 DVQD
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L20 ANSWER 26 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:872086 HCAPLUS
DN 136:32768
TI Nucleic acids and their encoded polypeptides from human tissues
IN Tang, Y. Tom; Liu, Chenghua; Drmanac, Radoje T.
PA Hyseq, Inc., USA
SO PCT Int. Appl., 831 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 124

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO2001088088	A2	20011122	2001WO-XB14827	20010516 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	WO2001088088	A2	20011122	2001WO-US14827	20010516 <--
	WO2001088088	A3	20021031		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRAI	2000US-0577408	A	20000518 <--		
	2001WO-US14827	W	20010516 <--		

AB The present invention provides a collection or library of 8051 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), standard PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human tissue sources and nearest neighbor sequence homologies are provided. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT 376373-52-3
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

RN 376373-52-3 HCAPLUS
CN Peptide, (Gln-Leu-Gln-Ala-Met-Ala-Ile-Phe-Glu-Tyr-Leu-Lys-Lys-Thr-Phe-Leu-

Arg-Pro-Gly-Thr-Val-Pro-His-Ser-Cys-Asn-Pro-Ser-Thr-Leu-Gly-Gly-Arg-Gly-Gly-Trp-Ile-Thr-Xaa-Gly-Gln-Glu-Leu-Glu-Ala-Ser-Pro) (9CI) (CA INDEX NAME)

SEQ 1 QLQAMAIFEY LKKTFLRPGT VPHSCNPSTL GGRGGWITXG QELEASP

L20 ANSWER 27 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:834397 HCAPLUS
DN 136:65028
TI Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
AU Kaneko, Takakazu; Nakamura, Yasukazu; Wolk, C. Peter; Kuritz, Tanya; Sasamoto, Shigemi; Watanabe, Akiko; Iriguchi, Mayumi; Ishikawa, Atsuko; Kawashima, Kumiko; Kimura, Takaharu; Kishida, Yoshie; Kohara, Mitsuyo; Matsumoto, Midori; Matsuno, Ai; Muraki, Akiko; Nakazaki, Naomi; Siumpo, Sayaka; Sugimoto, Masako; Takazawa, Masaki; Yamada, Manabu; Yasuda, Miho; Tabata, Satoshi
CS Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SO DNA Research (2001), 8(5), 205-213
CODEN: DARSE8; ISSN: 1340-2838
PB Universal Academy Press
DT Journal
LA English
AB The nucleotide sequence of the entire genome of a filamentous cyanobacterium, Anabaena sp. strain PCC 7120, was determined The genome of Anabaena consisted of a single chromosome (6,413,771 bp) and six plasmids, designated pCC7120α (408,101 bp), pCC7120β (186,614 bp), pCC7120γ (101,965 bp), pCC7120δ (55,414 bp), pCC7120ε (40,340 bp), and pCC7120ζ (5,584 bp). The chromosome bears 5368 potential protein-encoding genes, four sets of rRNA genes, 48 tRNA genes representing 42 tRNA species, and 4 genes for small structural RNAs. The predicted products of 45% of the potential protein-encoding genes showed sequence similarity to known and predicted proteins of known function, and 27% to translated products of hypothetical genes. The remaining 28% lacked significant similarity to genes for known and predicted proteins in the public DNA databases. More than 60 genes involved in various processes of heterocyst formation and nitrogen fixation were assigned to the chromosome based on their similarity to the reported genes. One hundred and ninety-five genes coding for components of two-component signal transduction systems, nearly 2.5-fold as many as those in Synechocystis sp. PCC 6803, were identified on the chromosome. Only 37% of the Anabaena genes showed significant sequence similarity to those of Synechocystis, indicating a high degree of divergence of the gene information between the two cyanobacterial strains.
IT **374860-51-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genomic sequence of filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120)
RN 374860-51-2 HCAPLUS
CN Cation transport ATPase (Nostoc sp. PCC 7120 gene all2908) (9CI) (CA INDEX NAME)

SEQ
1 MTATKPETSK QVAQKSSIIA GVAYSVVHTI PGRIRFRVPL VAHDLYYAQR
51 LQELLESDSH ILEVRVNPWA ASVAIRYEQS ASNRLIEAYL VGLLHQAKFR
101 QPSTVNRQQV TKSDNAGVKL PVLATVLAVL GLGFPIPRAI IAATVGLAAL
151 PVAKRAYTSI TQKRKLNIDC LDFIAIALTS AQGNLLTPAL VMTLHEIGDI
201 IRDRTARVTE NHAADLLASL GHYAWVAQPD GQKKRLLATQ VQPQDTVIVY
251 PGEQIPVDGQ ILRGKALIDQ QKLTGESMPV LRQVGEAVYA STLLREGEIY
301 IQAERVGTAT RAGASIELVQ QAPVHDTRMG NYAADIADQA ILPSLIFAGL
351 VFAATRNPAR AASILTLDFV TGIRVSLPTT FLAALHHATR HGVLIRSGRA

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401 LEKLAQVDTL VFDKTGTLTK GDIEVVEVEI IADRITTHRL IALATAAEQR
451 LTHPVAEAVV RYAEKQGIEI LPRQEFEYEI GLGVRAEIDG EQVIVGSDRF
501 LRQCGIPLDC LYEPHSCNHA DCPKHLNCRI SAHDSLLYVA VNQEFQGVIY
551 YTDPLRPESP AVIEKLQTEY GMEIHLLTGD NQQRAMAVAA ELHLPLFQVH
601 AEAFPAQKAE IIQKFHDSGK TVAFTGDGLN DSIALAYADV AISFGSGSEV
651 ARETADVVLM DDNLTSFLEA IAIARQTQAV IKQNISLAVV PNLAALGLAT
701 TVGIHPLAAT VVHNGSAIAA GLNGLRPLMH KDPPR
```

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Altschul, S	1997	25	3389	Nucl Acids Res	HCAPLUS
Bancroft, I	1989	171	5940	J Bacteriol	HCAPLUS
Bancroft, I	1989	171	5949	J Bacteriol	HCAPLUS
Bancroft, I	1988	16	7405	Nucleic Acids Res	HCAPLUS
Corry, M	1974	46	63	FEBS Lett	HCAPLUS
Delcher, A	1999	27	4636	Nucleic Acids Res	HCAPLUS
Duyvesteyn, M	1983	134	276	Arch Microbiol	HCAPLUS
Golden, J	1998		162	Bacterial genomes ph	HCAPLUS
Gorbalenya, A	1998	26	1741	Nucleic Acids Res	HCAPLUS
Gorodkin, J	2001	29	169	Nucleic Acids Res	HCAPLUS
Iwasaki, H	2000	41	1013	Plant Cell Physiol	HCAPLUS
Janda, L	1996	178	1487	J Bacteriol	HCAPLUS
Kaneko, T	1995	2	153	DNA Res	HCAPLUS
Kaneko, T	1996	3	109	DNA Res	HCAPLUS
Kumano, M	1983	24	219	Gene	HCAPLUS
Kuritz, T	1993	8	101	Mol Microbiol	HCAPLUS
Lambert, G	1984	781	45	Biochim Biophys Acta	HCAPLUS
Ligon, P	1991	19	4553	Nucleic Acids Res	HCAPLUS
Linden, H	1994	24	369	Plant Mol Biol	HCAPLUS
Lowe, T	1997	25	955	Nucleic Acids Res	HCAPLUS
Matveyev, A	2001	29	1491	Nucl Acids Res	HCAPLUS
Mizuno, T	1996	3	407	DNA Res	HCAPLUS
Motallebi-Veshareh, M	1990	4	1455	Mol Microbiol	HCAPLUS
Muro-Pastor, A	1994	176	1093	J Bacteriol	HCAPLUS
Muro-Pastor, A	1997	268	589	J Mol Biol	HCAPLUS
Neer, E	1994	371	297	Nature	HCAPLUS
Padhy, R	1988	170	1934	J Bacteriol	HCAPLUS
Pietrokovski, S	1996	12	287	Trends Genet	MEDLINE
Riley, M	1993	57	862	Microbiol Rev	HCAPLUS
Shizuya, H	1992	89	8794	Proc Natl Acad Sci	HCAPLUS
Simon, R	1978	136	414	J Bacteriol	HCAPLUS
van der Biezen, E	1998	8	226	Curr Biol	
Vioque, A	1992	20	6331	Nucleic Acids Res	HCAPLUS
Watanabe, T	1998	1396	97	Biophys Acta	HCAPLUS
Watanabe, T	1997	416	302	FEBS Lett	HCAPLUS
Wolk, C	2000		83	Prokaryotic developm	HCAPLUS
Wolk, C	1994		769	The molecular biolog	HCAPLUS
Wu, H	1998	95	9226	Proc Natl Acad Sci	HCAPLUS
Xu, M	1990	250	1566	Science	HCAPLUS
Xu, X	1997	179	2884	J Bacteriol	HCAPLUS

L20 ANSWER 28 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:828435 HCAPLUS
DN 137:42609
TI Human nucleic acids and polypeptides and their diagnostic and therapeutic uses
IN Drmanac, Rodoje T.; Liu, Chenghua; Tang, Y. Tom
PA Hyseq, Inc., USA
SO PCT Int. Appl., 103 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 124

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO2001075067	A2	20011011	2001WO-XA08631	20010330 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	WO2001075067	A2	20011011	2001WO-US08631	20010330 <--
	WO2001075067	A3	20020404		
	WO2001075067	C2	20021031		
	WO2001075067	C1	20041014		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRAI	2000US-0540217	A	20000331 <--		
	2000US-0649167	A	20000823 <--		
	2001WO-US08631	W	20010330 <--		

AB The present invention provides 30,368 nucleic acids and the 30,368 novel human polypeptide sequences encoded by these nucleic acids. A plurality of novel nucleic acids are obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosomes using standard PCR, sequencing by hybridization signature anal., and Sanger sequencing techniques. Nearest neighbor results are identified by sequence homol. searching. The invention also relates to therapeutic, diagnostic, and research utilities for these polynucleotides and proteins. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **437844-19-4**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; human nucleic acids and polypeptides and their diagnostic and therapeutic uses)

RN 437844-19-4 HCAPLUS

CN Protein (human clone WO0175067-SEQID-57487) (9CI) (CA INDEX NAME)

SEQ
```
  1 MRQDGKVARQ LLVIGEMVRQ RSAAGNKEGD KTPQPIPLTA QGSKPYQYHQ
 51 EGTPISAPKI KPVSIVGDKK QMDLSTVQKY ADGVATHNLD HASYHVEGDT
101 VPDMDPQWNY QRASQDLKCK NHMTEKVRNF KCERELAQGN STGFEMEGSR
151 GKDGLYELSG PQLTARKEVP HSCNCNKLNM ADDLNQLLIK ATPFTISVSP
201 VRGSSCYISW FPDRQARAVC GRPPWRINAV AEHREGTGTW HLESGRLKLV
251 CVWCERGVLS RGDTGQVQTK PTPLGTMLKN FKKEFKGDYG VTMIPGKLRT
301 LCEIDWPAFE GGNLAFLGDL KGCDELKNFQ ELINQSAIVH PQADVWWYCG
351 GPLLGTLPE
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L20 ANSWER 29 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2001:818860 HCAPLUS

DN 136:80679

TI Complete genome sequence of Salmonella enterica serovar typhimurium LT2

AU McClelland, Michael; Sanderson, Kenneth E.; Spleth, John; Clifton, Sandra W.; Latreille, Phil; Courtley, Laura; Porwolilk, Steffen; All, Johar; Daute, Mike; Du, Felyu; Hou, Shunfang; Layman, Dan; Leonard, Shawn; Nguyen, Christine; Scott, Kelsi; Holmes, Andrea; Grewal, Neenu; Mulvaney, Elizabeth; Ryan, Ellen; Sun, Hul; Florea, Lillana; Miller, Webb; Stoneking, Tamberiyn; Nhan, Michael; Waterston, Robert; Wilson, Richard K.

CS Sidney Kimmel Cancer Center, San Diego, CA, 92121, USA

SO Nature (London, United Kingdom) (2001), 413(6858), 852-856
CODEN: NATUAS; ISSN: 0028-0836

PB Nature Publishing Group

DT Journal

LA English

AB Salmonella enterica subspecies I, serovar typhimurium (S. typhimurium), is a leading cause of human gastroenteritis, and is used as a mouse model of human typhoid fever. The incidence of non-typhoid salmonellosis is increasing worldwide, causing millions of infections and many deaths in the human population each year. The 4857-kilobase (kb) chromosome and 94-kb virulence plasmid of S. typhimurium strain LT2 has now been sequenced.. The distribution of close homologs of S. typhimurium LT2 genes in 8 related enterobacteria was determined using previously completed genomes of 3 related bacteria, sample sequencing of both S. enterica serovar paratyphi A (S. paratyphi A) and Klebsiella pneumoniae, and hybridization of 3 unsequenced genomes to a microarray of S. typhimurium LT2 genes. Lateral transfer of genes is frequent, with 11% of the S. typhimurium LT2 genes missing from S. enterica serovar Typhi (S. typhi), and 29% missing from Escherichia coli K12. The 352 gene homologs of S. typhimurium LT2 confined to subspecies I of S. enterica - containing most mammalian and bird pathogens - are useful for studies of epidemiol., host specificity, and pathogenesis. Most of these homologs were previously unknown, and 50 may be exported to the periplasm or outer membrane, rendering them accessible as therapeutic or vaccine targets. The sequences are available from the GenBank database under Accession Nos. AE006468 (chromosome) and AE006471 (pSTL).

IT **384930-08-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Salmonella enterica serovar typhimurium LT2)

RN 384930-08-9 HCAPLUS

CN GDP-D-mannose dehydratase in colanic acid gene cluster (Salmonella enterica typhimurium strain LT2; SGSC 1412; ATCC 700720 gene gmd) (9CI) (CA INDEX NAME)

SEQ
```
  1 MSKVALITGV TGQDGSYLAE FLLEKGYEVH GIKRRASSFN TERVDHIYQD
 51 PHSCNPKFHL HYGDLTDASN LTRILQEVQP DEVYNLGAMS HVAVSFESPE
101 YTADVDAMGT LRLLEAIRFL GLEKKTRFYQ ASTSELYGLV QEIPQKETTP
151 FYPRSPYAVA KLYAYWITVN YRESYGIYAC NGILFNHESP RRGETFVTRK
201 ITRAIANIAQ GLESCLYLGN MDSLRDWGHA KDYVRMQWMM LQQEQPEDFV
251 IATGVQYSVR QFVELAAAQL GIKLRFEGEG INEKGIVVSV TGHDAPGVKP
301 GDVIVAVDPR YFRPAEVETL LGDPSKAHEK LGWKPEITLS EMVSEMVAND
351 LEAAKKHSLL KSHGYEVAIA LES
```

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ahmer, B	1999	181	1364	J Bacteriol	HCAPLUS
Anon	1996			Cellular and Molecul	
Bermudes, D	2000	465	57	Adv Exp Med Biol	MEDLINE
Blanc-Potard, A	1999	181	998	J Bacteriol	HCAPLUS
Blattner, F	1997	277	1453	Science	HCAPLUS
Bumann, D	2000	27	357	FEMS Immunol Med Mic	HCAPLUS
Chalker, R	1988	10	111	Rev Infect Dis	MEDLINE

Cooke, E	1990	336	790	Lancet	MEDLINE
Decker, K	1999	32	777	Mol Microbiol	HCAPLUS
Figueroa-Bossi, N	2001	39	260	Mol Microbiol	HCAPLUS
Florea, L	2000	28	3486	Nucleic Acids Res	HCAPLUS
Gupta, S	1995	177	4207	J Bacteriol	HCAPLUS
Lan, R	1996	13	47	Mol Biol Evol	HCAPLUS
Liu, S	1993	175	4104	J Bacteriol	HCAPLUS
Liu, S	1996	93	10303	Proc Natl Acad Sci	HCAPLUS
Matsui, H	2001	183	4652	J Bacteriol	HCAPLUS
McClelland, M	2000	28	4974	Nucleic Acids Res	HCAPLUS
Nakai, K	1999	24	34	Trends Biochem Sci	HCAPLUS
Ochman, H	2000	405	299	Nature	HCAPLUS
Parkhill, J	2001	413	848	Nature	HCAPLUS
Perna, N	2001	409	529	Nature	HCAPLUS
Pizza, M	2000	287	1816	Science	HCAPLUS
Popoff, M	2000	151	893	Res Microbiol	HCAPLUS
Porwollik, S	2001	483	1	Mut Res	HCAPLUS
Reidl, J	1991	173	4862	J Bacteriol	HCAPLUS
Selander, R	1996		2691	Cellular and Molecul	
Stanley, T	2000	182	4406	J Bacteriol	HCAPLUS
Tatusov, R	2001	29	22	Nucleic Acids Res	HCAPLUS
Todd, E	1990	336	788	Lancet	MEDLINE
Townsend, S	2001	69	2894	Infect Immun	HCAPLUS

L20 ANSWER 30 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:818857 HCAPLUS
DN 136:15814
TI Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi CT18
AU Parkhill, J.; Dougan, G.; James, K. D.; Thomson, N. R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K. L.; Bentley, S. D.; Holden, M. T. G.; Sebalhia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R. M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T. T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T. S.; Leather, S.; Moule, S.; O'Gaora, P.; Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B. G.
CS The Sanger Centre, Wellcome Trust Genome Campus, Cambridge, CBIO ISA, UK
SO Nature (London, United Kingdom) (2001), 413(6858), 848-852
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB Salmonella enterica serovar typhi (S. typhi) is the etiol. agent of typhoid fever, a serious invasive bacterial disease of humans with an annual global burden of .apprx.16 million cases, leading to 600,000 fatalities. Many S. enterica serovars actively invade the mucosal surface of the intestine but are normally contained in healthy individuals by the local immune defense mechanisms. However, S. typhi has evolved the ability to spread to the deeper tissues of humans, including liver, spleen, and bone marrow. The 4,809,037-bp genome was sequenced for a S. typhi (CT18) that is resistant to multiple drugs, revealing the presence of hundreds of insertions and deletions compared with the Escherichia coli genome, ranging in size from single genes to large islands. Notably, the genome sequence identifies >200 pseudogenes, several corresponding to genes that are known to contribute to virulence in Salmonella typhimurium. This genetic degradation may contribute to the human-restricted host range for S. typhi. CT18 harbors a 218,150-bp multiple-drug-resistance IncH1 plasmid (pHCM1), and a 106,516-bp cryptic plasmid (pHCM2), which shows recent common ancestry with a virulence plasmid of Yersinia pestis.
IT **372050-75-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi CT18)
RN 372050-75-4 HCAPLUS

CN GDP-mannose 4,6-dehydratase (Salmonella enterica typhi strain CT18 gene STY2321) (9CI) (CA INDEX NAME)

SEQ
```
      1 MSKVALITGV TGQDGSYLAE FLLEKGYEVH GIKRRASSFN TERVDHIYQD
     51 PHSCNPKFHL HYGDLTDASN LTRILQEVQP DEVYNLGAMS HVAVSFESPE
    101 YTADVDAMGT LRLLEAIRFL GLEKKTRFYQ ASTSELYGLV QEIPQKETTP
    151 FYPRSPYAVA KLYAYWITVN YRESYGIYAC NGILFNHESP RRGETFVTRK
    201 ITRAIANIAQ GLESCLYLGN MDSLRDWGHA KDYVRMQWMM LQQEQPEDFV
    251 IATGVQYSVR QFVELAAAQL GIKLRFEGEG INEKGIVVSV TGHDAPGVKP
    301 RDVIVAVDPC YFRPAEVETL LGDPSKAHEK LGWKPEITLS EMVSEMVAND
    351 LEAAKKHSLL KSHGYEVAIA LES
```

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Bakshi, C	2000	182	2341	J Bacteriol	HCAPLUS
Blanc-Potard, A	1999	181	998	J Bacteriol	HCAPLUS
Blattner, F	1997	277	1453	Science	HCAPLUS
Doolittle, R	1996	271	470	Science	HCAPLUS
Hashimoto, Y	1993	175	4456	J Bacteriol	HCAPLUS
Hensel, M	1999	32	275	Mol Microbiol	HCAPLUS
Hu, P	1998	180	5192	J Bacteriol	HCAPLUS
Ivanhoff, B	1995	26	1	Southeast Asian J Tr	
Jing, D	1999	274	27287	J Biol Chem	HCAPLUS
Kingsley, R	2000	36	1006	Mol Microbiol	HCAPLUS
Marcus, S	2000	2	145	Microbes Infect	HCAPLUS
McClelland, M	2001	413	852	Nature	HCAPLUS
Miao, E	2000	97	7539	Proc Natl Acad Sci U	HCAPLUS
Mirold, S	1999	96	9845	Proc Natl Acad Sci U	HCAPLUS
Neidhardt, F	1996			Escherichia coli and	
Parkhill, J	2000	404	502	Nature	HCAPLUS
Parry, C	1998	351	1289	Lancet	MEDLINE
Perna, N	2001	409	529	Nature	HCAPLUS
Perry, R	1997	10	35	Clin Microbiol Rev	HCAPLUS
Prentice, M	2001	183	2586	J Bacteriol	HCAPLUS
Reeves, M	1989	27	313	J Clin Microbiol	HCAPLUS
Rosenberg, S	1994	265	405	Science	HCAPLUS
Rutherford, K	2000	16	944	Bioinformatics	HCAPLUS
Sanderson, K	1998	19	569	Electrophoresis	HCAPLUS
Sherburne, C	2000	28	2177	Nucleic Acids Res	HCAPLUS
Townsend, S	2001	69	2894	Infect Immun	HCAPLUS
Tsolis, R	1999	67	6385	Infect Immun	HCAPLUS
Wain, J	1998	36	1683	J Clin Microbiol	MEDLINE
Wong, K	1998	66	3365	Infect Immun	HCAPLUS
Zhang, X	2000	68	3067	Infect Immun	HCAPLUS

L20 ANSWER 31 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:672668 HCAPLUS
DN 135:328136
TI Human reproductive tract-specific nucleic acids and their encoded proteins and antibodies
IN Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.
PA Human Genome Sciences, Inc., USA
SO PCT Int. Appl., 1297 pp.
CODEN: PIXXD2
DT Patent
LA English

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO2001055320 A2		20010802	2001WO-US01339	20010117

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID,

IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB,
GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR

PRAI US 2000-PV179065 20000131
US 2000-PV180628 20000204
US 2000-PV184664 20000224
US 2000-PV186350 20000302
US 2000-PV189874 20000316
US 2000-PV190076 20000317
US 2000-PV198123 20000418
US 2000-PV205515 20000519
US 2000-PV209467 20000607
US 2000-PV214886 20000628
US 2000-PV215135 20000630
US 2000-PV216647 20000707
US 2000-PV216880 20000707
US 2000-PV217487 20000711
US 2000-PV217496 20000711
US 2000-PV218290 20000714
US 2000-PV220963 20000726
US 2000-PV220964 20000726
US 2000-PV225757 20000814
US 2000-PV225270 20000814

AB The present invention relates to novel reproductive tract-related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "reproductive tract antigens", and the use of such reproductive tract antigens for detecting disorders of the reproductive tract, particularly the presence of reproductive tract cancer and reproductive tract cancer metastases. More specifically, 2650 isolated reproductive tract-associated cDNA mols. are provided encoding novel reproductive tract-associated polypeptides. Novel reproductive tract polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human reproductive tract associated polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosis, treatment, prophylaxis, and/or prognosis of disorders related to the reproductive tract, including reproductive tract cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the production and function of the polypeptides of the present invention. [This abstract record is the second of three records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **367539-41-1P**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; human reproductive tract-specific nucleic acids and their encoded proteins and antibodies)

RN 367539-41-1 HCAPLUS
CN Reproductive tract-specific antigen (human clone HEQBE71 fragment) (9CI) (CA INDEX NAME)

SEQ 1 ILDPPPLPSA RWDAHVLERN RSEEPGPLGP SWLSGPQVMY SGLATNSGIL
51 GTPGTGWDCC PHSCNQQIFX APCLCQTADR RDTVVTKTXL LLGKSPERVQ
101 GETATSPVRR RGTXDRF

L20 ANSWER 32 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:208901 HCAPLUS
DN 134:217895
TI Functional annotation of a full-length mouse cDNA collection
AU Kawai, J.; Shinagawa, A.; Shibata, K.; Yoshino, M.; Itoh, M.; Ishii, Y.; Arakawa, T.; Hara, A.; Fukunishi, Y.; Konno, H.; Adachi, J.; Fukuda, S.; Aizawa, K.; Izawa, M.; Nishi, K.; Kiyosawa, H.; Kondo, S.; Yamanaka, I.; Saito, T.; Okazaki, Y.; Gojobori, T.; Bono, H.; Kasukawa, T.; Saito, R.; Kadota, K.; Matsuda, H.; Ashburner, M.; Batalov, S.; Casavant, T.; Fleischmann, W.; Gaasterland, T.; Gissi, C.; King, B.; Kochiwa, H.; Kuehl, P.; Lewis, S.; Matsuo, Y.; Nikaido, I.; Pesole, G.; Quackenbush, J.; Schriml, L. M.; Staubli, F.; Suzuki, R.; Tomita, M.; Wagner, L.; Washio, T.; Sakai, K.; Okido, T.; Furuno, M.; Aono, H.; Baldarelli, R.; Barsh, G.; Blake, J.; Boffelli, D.; Bojunga, N.; Carninci, P.; de Bonaldo, M. F.; Brownstein, M. J.; Bult, C.; Fletcher, C.; Fujita, M.; Gariboldi, M.; Gustincich, S.; Hill, D.; Hofmann, M.; Hume, D. A.; Kamiya, M.; Lee, N. H.; Lyons, P.; Marchionni, L.; Mashima, J.; Mazzarelli, J.; Mombaerts, P.; Nordone, P.; Ring, B.; Ringwald, M.; Rodriquez, I.; Sakamoto, N.; Sasaki, H.; Sato, K.; Schonbach, C.; Seya, T.; Shibata, Y.; Storch, K.-F.; Suzuki, H.; Toyo-oka, K.; Wang, K. H.; Weitz, C.; Whittaker, C.; Wilming, L.; Wynshaw-Boris, A.; Yoshida, K.; Hasegawa, Y.; Kawaji, H.; Kohtsuki, S.
CS The RIKEN Genome Exploration Res. Group Phase II Team, Lab. Genome Exploration Res. Group, RIKEN Genomic Sciences Center (GSC), Yokohama Inst., Yokohama, Kanagawa, 230-0045, Japan; The FANTOM Consortium
SO Nature (London) (2001), 409(6821), 685-690
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB The RIKEN Mouse Gene Encyclopaedia Project, a systematic approach to determining the full coding potential of the mouse genome, involves collection and sequencing of full-length cDNAs and phys. mapping of the corresponding genes to the mouse genome. An international functional annotation meeting (FANTOM) was organized to annotate the first 21,076 cDNAs to be analyzed in this project. This report describes the first RIKEN clone collection, which is one of the largest described for any organism. Anal. of these cDNAs extends known gene families and identifies new ones. The sequences are deposited into GenBank with Accession nos. AK002213-AK021412 and AK027261-AK027262. Information about these clones is available at RIKEN (http://www.gsc.riken.go.jp/e/FANTOM/viewer/) and Mouse Genome Informatics (http://www.informatics.jax.org and mirror sites). [This abstract record is the sixth of 7 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT 326053-89-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; functional annotation of a full-length mouse cDNA collection)
RN 326053-89-8 HCAPLUS
CN Protein (mouse strain C57BL/6J clone 1300017N15 818-amino acid) (9CI) (CA INDEX NAME)

SEQ
```
  1 MAEAPPVSGT FKFNTDAAEF IPQERKTSGL NCGTQRRLDS SRIGRRNYSS
 51 SPPCHLPRHI PYEDISAVHQ HSYASGSKPK SPQGFFQSSN KSLKNHGLQN
101 QPWQKARNEK HQNRNKKAQG LSEQTSDTSS LESVARSESG TNPREHSPSE
151 SEKEVVIADP RGAKPKKAAQ LTYNYGRGPK AKGRLRSEWG NRMSPKSEDE
201 NTRPVAISHT DSSDASCRKP VVDPCVCRRN EQRRYPQKRP PWEVEGARPR
251 PGRNPPKQES QRHINAGPKT NMSPIPKDNL RERPTKSACD TGNLAVVSKS
301 SRRVNQEKTA VRRQDPQVLS PFPRGKQNHM LKNVETHTGS LIEQLTTEKY
351 ECMVCCELVQ VTAPVWSCQS CFHVFHLNCI KKWARSPASH ADGQSGWRCP
401 ACQNVSAHVP NTYTCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS
451 CNLLCHPGPC PPCPAFTTKT CECGRTRHTV RCGQPVSVHC SNACENILNC
501 GQHHCAELCH GGQCQPCRII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS
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551 CLKICGKDLK CGSHTCSQVC HPQPCQPCPR LPHLVRYCPC GQTPLSQLLE
601 HGSNARKTCM DPVPSCGKVC GKPLACGSSD FIHTCEKLCH EGDCGPCSRT
651 SVISCRCSFR TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD
701 KEHKCPLICG RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY
751 PPVPCGTRPP ECTQTCARIH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK
801 HEELTIKKLW TFKETLDF

L20 ANSWER 33 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:166626 HCAPLUS
DN 134:363141
TI LEPS2, a phosphorus starvation-induced novel acid phosphatase from tomato
AU Baldwin, James C.; Karthikeyan, Athikkattuvalasu S.; Raghothama, Kashchandra G.
CS Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN, 47907-1165, USA
SO Plant Physiology (2001), 125(2), 728-737
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal
LA English
AB Phosphate (Pi) is one of the least available plant nutrients found in the soil. A significant amount of phosphate is bound in organic forms in the rhizosphere. Phosphatases produced by plants and microbes are presumed to convert organic phosphorus into available Pi, which is absorbed by plants. In this study we describe the isolation and characterization of a novel tomato (Lycopersicon esculentum) phosphate starvation-induced gene (LePS2) representing an acid phosphatase. LePS2 is a member of a small gene family in tomato. The cDNA is 942 bp long and contains an open reading frame encoding a 269-amino acid polypeptide. The amino acid sequence of LePS2 has a significant similarity with a phosphatase from chicken. Distinct regions of the peptide also share significant identity with the members of HAD and DDDD super families of phosphohydrolases. Many plant homologs of LePS2 are found in the databases. The LePS2 transcripts are induced rapidly in tomato plant and cell culture in the absence of Pi. However, the induction is repressible in the presence of Pi. Divided root studies indicate that internal Pi levels regulate the expression of LePS2. The enhanced expression of LePS2 is a specific response to Pi starvation, and it is not affected by starvation of other nutrients or abiotic stresses. The bacterially (Escherichia coli) expressed protein exhibits phosphatase activity against the synthetic substrate p-nitrophenyl phosphate. The pH optimum of the enzyme activity suggests that LePS2 is an acid phosphatase.
IT 340053-32-9P, Phosphatase, acid (tomato gene LePS2)
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process)
(amino acid sequence; cloning, sequence and expression of LEPS2, a phosphorus starvation-induced novel acid phosphatase from tomato)
RN 340053-32-9 HCAPLUS
CN Phosphatase, acid (tomato gene LePS2) (9CI) (CA INDEX NAME)

SEQ 1 MAGIVVVFDF DKTIIEVDSD NWVVDELGAT DLFNQLLPTM PWNSLMDRMM
51 KELHTQGKTI QDIEEVLKRV PIHPRIVPAI KSAHALGCDL RVISDANVFF
101 IETILKHLGI RDCFSEINTN PGYVDGEGRL RILPYVDFQK SPHSCNLCPP
151 NMCKGMIVER IQAKEGKKRM IYLGDGIGDF CPSLKLREAD FVMPRKDFPA
201 WNLINKNRTL VKAGVHEWTN GKELEHILLQ WINTINIEES QLLSMENCKF
251 QTKHNAAHGA LPRPLPVPY

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Altschul, S	1990	215	403	J Mol Biol	HCAPLUS
Aravind, L	1998	23	127	Trends Biochem Sci	HCAPLUS
Ascencio, J	1994	25	1553	Commun Soil Sci Plan	HCAPLUS
Baldwin, J	1999	99	S-190	Plant Physiol	
Barber, S	1980		591	Role of Phosphorus i	
Barret-Lennard, E	1982	33	682	J Exp Bot	
Bose, S	1998	250	629	Biochem Biophys Res	HCAPLUS
Bosse, D	1998	21	325	Plant Cell Environ	HCAPLUS
Boutin, J	1981	51	353	Physiol Plant	HCAPLUS
Bressan, R	1981	21	23	Plant Sci Lett	HCAPLUS
Collet, J	1998	273	14107	J Biol Chem	HCAPLUS
Dellaporta, S	1983	1	19	Plant Mol Biol Rep	HCAPLUS
Denecke, J	1990	2	51	Plant Cell	HCAPLUS
Drew, M	1984	160	500	Planta	HCAPLUS
Duff, S	1994	90	791	Physiol Plant	HCAPLUS
Duff, S	1989	90	1275	Plant Physiol	HCAPLUS
Goldstein, A	1988	87	711	Plant Physiol	HCAPLUS
Goldstein, A	1988	87	716	Plant Physiol	HCAPLUS
Houston, B	1999	1448	500	Biochem Biophys Acta	HCAPLUS
Hubel, F	1996	112	1429	Plant Physiol	
Jones, J	1982	5	1005	J Plant Physiol	
Jungk, A	1993	155/1	91	Plant Soil	
Lefebvre, D	1982	54	199	Physiol Plant	HCAPLUS
Lefebvre, D	1990	93	504	Physiol Plant	HCAPLUS
Li, M	1996	42	753	Soil Sci Plant Nutr	
Liu, C	1996	33	867	Plant Mol Biol	
Liu, C	1998	116	91	Plant Physiol	HCAPLUS
Muchhal, U	1996	93	10519	Proc Natl Acad Sci U	HCAPLUS
Muchhal, U	1999	96	5868	Proc Natl Acad Sci U	HCAPLUS
Ozawa, K	1995	41	461	Soil Sci Plant Nutr	HCAPLUS
Pan, S	1987	14	117	Aust J Plant Physiol	HCAPLUS
Pawlowski, K	1994		1	Plant Molecular Biol	
Plaxton, W	1999		349	Plant Responses to E	HCAPLUS
Raghothama, K	1999	50	665	Annu Rev Plant Physi	HCAPLUS
Raghothama, K	2000	3	182	Curr Opin Plant Biol	HCAPLUS
Richardson, A	1994		50	Soil Biota Managemen	
Sambrook, J	1989			Molecular Cloning: A	
Shimogawara, K	1995	36	341	Plant Cell Physiol	HCAPLUS
Sigma Diagnostics	1985			Phosphatase, alkalin	
Thaller, M	1998	7	1651	Protein Sci	
Thompson, J	1997	24	4876	Nucleic Acids Res	
Todano, T	1994	9	521	Trans 15th World Con	
Trull, M	1998	206	544	Planta	HCAPLUS
Ueki, K	1971	24	506	Physiol Plant	
Wasaki, J	1999	45	439	Soil Sci Plant Nutr	HCAPLUS

L20 ANSWER 34 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:106057 HCAPLUS
DN 134:188987
TI Human expressed sequence tags and primers for synthesizing full-length cDNAs
IN Ota, Toshio; Isogai, Takao; Nishikawa, Tetsuo; Hayashi, Kohji; Saito, Kaoru; Yamamoto, Junichi; Ishii, Shizuko; Sugiyama, Tomoyasu; Wakamatsu, Ai; Nagai, Keiichi; Otsuki, Tetsuji
PA Helix Research Institute, Japan
SO Eur. Pat. Appl., 2527 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 12

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP---1074617	A2	20010207	2000EP-0116126	20000728 <--

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     JP2002171977          A2    20020618    2000JP-0196309          20000626 <--
     CA---2380472          AA    20010208    2000CA-2380472          20000728 <--
     EP---1205549          A1    20020515    2000EP-0948282          20000728 <--
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, SI, LT, LV, FI, RO, MK, CY, AL
     JP2002191363          A2    20020709    2000JP-0280990          20000728 <--
PRAI 1999JP-0248036        A     19990729  <--
     1999JP-0300253        A     19990827  <--
     2000JP-0118776        A     20000111  <--
     2000JP-0183767        A     20000502  <--
     2000JP-0241899        A     20000609  <--
     1999US-159590P        P     19991018  <--
     2000US-183322P        P     20000217  <--
     2000WO-JP05065        W     20000728  <--
AB   Primers for synthesizing full-length cDNAs and their use are provided.
     The invention provides 5'-end sequences for 5602 partial cDNA sequences
     (expressed sequence tags, ESTs) and 3'-end sequences for 4970 of these
     clones.  Furthermore, primers for synthesizing the full-length cDNA have
     been provided to clarify the function of the protein encoded by the cDNA.
     The full-length cDNA sequences s of the present invention containing the
     translation start site provides information useful for analyzing the
     functions of the proteins.  Tissue- and cell-specific expression patterns
     are also provided.  [This abstract record is one of 6 records for this
     patent necessitated by the large number of index entries required to fully
     index the document and publication system constraints.].
IT   327117-94-2, Protein (human clone PLACE1010310)
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study)
        (amino acid sequence; human expressed sequence tags and primers for
        synthesizing full-length cDNAs)
RN   327117-94-2  HCAPLUS
CN   Protein (human clone PLACE1010310) (9CI)  (CA INDEX NAME)

SEQ      1 MSDSPAGSNP RTPESSGSGS GGGGKRPAVP AAVSLLPPAD PLRQANRLPI
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       101 KPDPPPSSKL NSVAAAANGL GAEKDPGRSA PGAASAAAAL KQLGDSPAED
       151 KSSFKPYSKG SGGGDSRKDS GSSSVSSTSS SSSSSPGDKA GFRVPSAACP
       201 PFPPHGAPVS ASSSSSSPGG SRGGSPHHSD CKNGGGVGGG ELDKKDQEPK
       251 PSPEPAAVSR GGGGEPGAHG GAESGASGRK SEPPSALVGA GHVAPVSPYK
       301 PGHSVFPLPP SSIGYHGSIV GAYAGYPSQF VPGLDPSKSG LVGGQLSGGL
       351 GLPPGKPPSS SPLTGASPPS FLQGLCRDPY CLGGYHGASH LGGSSCSTCS
       401 AHDPAGPSLK AGGYPLVYPG HPLQPAALSS SAAQAALPGH PLYTYGFMLQ
       451 NEPLPHSCNW VAASGPCDKR FATSEELLSH LRTHTALPGA EKLLAAYPGA
       501 SGLGSAAAAA AAAASCHLHL PPPAAPGSPG SLSLRNPHTL GLSRYHPYGK
       551 SHLSTAGGLA VPSLPTAGPY YSPYALYGQR LASASALGYQ


L20  ANSWER 35 OF 42  HCAPLUS  COPYRIGHT 2006 ACS on STN
AN   2000:824291  HCAPLUS
DN   134:21425
TI   Protection of endogenous therapeutic peptides from peptidase activity
     through conjugation to blood components
IN   Bridon, Dominique P.; Ezrin, Alan M.; Milner, Peter G.; Holmes, Darren L.;
     Thibaudeau, Karen
PA   Conjuchem, Inc., Can.
SO   PCT Int. Appl., 733 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 5
     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
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                WO2000069900          A3     20010215
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                        CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
                        IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
                        MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
                        SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
                    RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
                        DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
                        CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
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                CA---2373680          AA     20001123    2000CA-2373680          20000517 <--
                CA---2499211          AA     20001123    2000CA-2499211          20000517 <--
                CA---2501421          AA     20001123    2000CA-2501421          20000517 <--
                CA---2505617          AA     20001123    2000CA-2505617          20000517 <--
                WO2000070665          A2     20001123    2000WO-IB00763          20000517 <--
                WO2000070665          A3     20010419
                    W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
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                        IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
                        MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
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                    RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ,
                        MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
                        IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML,
                        MR, NE, SN, TD, TG
                EP---1105409          A2     20010613    2000EP-0936023          20000517 <--
                EP---1105409          B1     20060301
                    R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
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                EP---1264840          A1     20021211    2002EP-0014617          20000517 <--
                    R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
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                JP2003508350          T2     20030304    2000JP-0618316          20000517 <--
                AU----765753          B2     20030925    2000AU-0051393          20000517 <--
                EP---1591453          A1     20051102    2005EP-0105384          20000517 <--
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                US---6849714          B1     20050201    2000US-0623548          20000905 <--
                US---6514500          B1     20030204    2000US-0657332          20000907 <--
                ZA2001006676          A      20020719    2001ZA-0006676          20010814 <--
                ZA2001009110          A      20020613    2001ZA-0009110          20011105 <--
                US2003108567          A1     20030612    2002US-0287892          20021104 <--
                US---6821949          B2     20041123
                US2003108568          A1     20030612    2002US-0288340          20021104 <--
                US---6887849          B2     20050503
                US2004127398          A1     20040701    2003US-0722733          20031125 <--
                US2004138100          A1     20040715    2003US-0723099          20031125 <--
                US2005176641          A1     20050811    2005US-0040810          20050121 <--
                US2005176643          A1     20050811    2005US-0067556          20050225 <--
                JP2005263807          A2     20050929    2005JP-0115175          20050412 <--
                JP2005239736          A2     20050908    2005JP-0140407          20050512 <--
                JP2005255689          A2     20050922    2005JP-0151458          20050524 <--
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	US2006009377	A1	20060112	2005US-0170967	20050629 <--
	US2006058235	A1	20060316	2005US-0215967	20050830 <--
PRAI	1999US-134406P	P	19990517	<--	
	1999US-153406P	P	19990910	<--	
	1999US-159783P	P	19991015	<--	
	2000CA-2363712	A3	20000517	<--	
	2000CA-2373680	A3	20000517	<--	
	2000EP-0932570	A3	20000517	<--	
	2000EP-0936023	A3	20000517	<--	
	2000JP-0618316	A3	20000517	<--	
	2000JP-0618327	A3	20000517	<--	
	2000WO-IB00763	W	20000517	<--	
	2000WO-US13576	W	20000517	<--	
	2000US-0623548	A1	20000905	<--	
	2000US-0657276	A2	20000907	<--	
	2000US-0657332	A3	20000907	<--	
	2002US-400199P	P	20020731	<--	
	2002US-400413P	P	20020731	<--	
	2002US-0288340	A1	20021104	<--	
	2003WO-CA01097	W	20030729		
	2003US-0471348	B1	20030908		
	2003US-0722733	A1	20031125		
	2005US-0040810	A2	20050121		
	2005US-0170967	A1	20050629		

AB A method for protecting a peptide from peptidase activity in vivo, the peptide being composed of between 2 and 50 amino acids and having a C-terminus and an N-terminus and a C-terminus amino acid and an N-terminus amino acid is described. In the first step of the method, the peptide is modified by attaching a reactive group to the C-terminus amino acid, to the N-terminus amino acid, or to an amino acid located between the N-terminus and the C-terminus, such that the modified peptide is capable of forming a covalent bond in vivo with a reactive functionality on a blood component. The solid phase peptide synthesis of a number of derivs. with 3-maleimidopropionic acid (3-MPA) is described. In the next step, a covalent bond is formed between the reactive group and a reactive functionality on a blood component to form a peptide-blood component conjugate, thereby protecting said peptide from peptidase activity. The final step of the method involves the analyzing of the stability of the peptide-blood component conjugate to assess the protection of the peptide from peptidase activity. Thus, the percentage of a K5 kringle peptide (Pro-Arg-Lys-Leu-Tyr-Asp-Lys-NH2) conjugated to human serum albumin via MPA remained relatively constant through a 24-h plasma assay in contrast to unmodified K5 which decreased to 9% of the original amount of K5 in only 4 h in plasma.

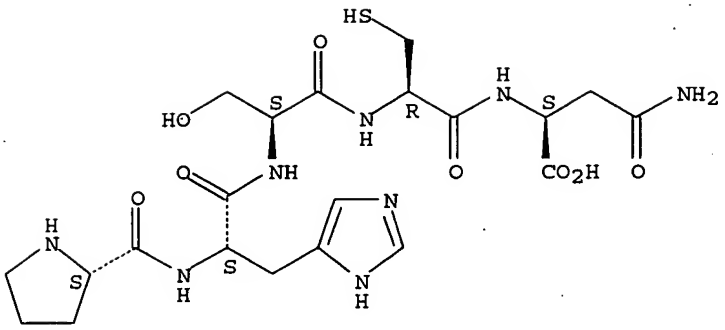
IT **252229-85-9**
RL: PRP (Properties)
(unclaimed sequence; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

RN 252229-85-9 HCAPLUS

CN L-Asparagine, L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

SEQ 1 PHSCN

Absolute stereochemistry.



L20 ANSWER 36 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:660998 HCAPLUS
DN 134:217856
TI The colanic acid gene cluster of Salmonella enterica has a complex history
AU Stevenson, G.; Lan, R.; Reeves, P. R.
CS Department of Microbiology (G08), University of Sydney, Sydney, N.S.W., 2006, Australia
SO FEMS Microbiology Letters (2000), 191(1), 11-16
CODEN: FMLED7; ISSN: 0378-1097
PB Elsevier Science B.V.
DT Journal
LA English
AB The colanic acid gene cluster of Salmonella enterica LT2 was sequenced and compared with that of Escherichia coli K-12. The two clusters are similar with divergence slightly higher than average for genes of the two species. The cluster was divided into four blocks by GC content and seems likely to have transferred from a higher GC content species to the ancestor of E. coli and S. enterica. All 19 genes of K-12 and 13 genes of LT2 appear to have undergone random genetic drift with amelioration of the GC content. However, in the case of S. enterica, we believe that the six genes of the GDP-fucose pathway group were replaced relatively recently by genes closely related to those of the original donor species. Two repetitive elements were observed: a bacterial interspersed mosaic element in the intergenic region between wzx and wcaK in K-12 only and a RSA (repetitive sequence element) sequence between wcaJ and wzx in LT2 only.
IT **329379-69-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; colanic acid gene cluster of Salmonella enterica has a complex history)
RN 329379-69-3 HCAPLUS
CN Dehydratase, guanosine diphosphomannose 4,6- (Salmonella typhimurium strain LT2 gene gmd) (9CI) (CA INDEX NAME)

SEQ
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  1 MSKVALITGV TGQDGSYLAE FLLEKGYEVH GIKRRASSFN TERVDHIYQD
 51 PHSCNPKFHL HYGDLTDASN LTRILQEVQP DEVYNLGAMS HVAVSFESPE
101 YTADVDAMGT LRLLEAIRFL GLEKKTRFYQ ASTSELYGLV QEIPQKETTP
151 FYPRSPYAVA KLYAYWITVN YRESYGIYAC NGILFNHESP RRGETFVTRK
201 ITRAIANIAQ GLESCLYLGN MDSLRDWGHA KDYVRMQWMM LQQEQPEDFV
251 IATGVQYSVR QFVELAAAQL GIKLRFEGEG INEKGIVVSV TGHDAPGVKP
301 GDVIVAVDPR YFRPAEVETL LGDPSKAHEK LGWKPEITLS EMVSEMVAND
351 LEAAKKHSLL KSHGYEVAIA LES
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Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File

Aoyama, K	1994	11	829	Mol Biol Evol	HCAPLUS
Bachellier, S	1996	2	2012	Escherichia and Salm	
Bachellier, S	1997	145	551	Genetics	HCAPLUS
Frick, D	1995	270	24086	J Biol Chem	HCAPLUS
Gleeson, T	1991	7	398	Comput Appl Biosci	MEDLINE
Hobbs, M	1994	12	855	Mol Microbiol	HCAPLUS
Jiang, X	1991	5	695	Mol Microbiol	HCAPLUS
Lawrence, J	1997	44	383	J Mol Evol	HCAPLUS
Lee, S	1992	138	1843	J Gen Microbiol	HCAPLUS
Marolda, C	1993	175	148	J Bacteriol	HCAPLUS
Reeves, P	1994	10	281	CABIOS	HCAPLUS
Reeves, P	1996	4	495	Trends Microbiol	MEDLINE
Sharp, P	1987	4	222	Mol Biol Evol	HCAPLUS
Stevenson, G	1994	176	4144	J Bacteriol	HCAPLUS
Stevenson, G	1996	178	4885	J Bacteriol	HCAPLUS
Stevenson, G	1991	227	173	Mol Gen Genet	HCAPLUS
Sueoka, N	1962	48	582	Proc Natl Acad Sci	HCAPLUS
Sueoka, N	1988	85	2653	Proc Natl Acad Sci	HCAPLUS
Wang, L	1998	66	3545	Infect Immun	HCAPLUS
Wang, L	1998	36	3182	J Clin Microbiol	HCAPLUS
Zhang, L	1997	23	63	Mol Microbiol	HCAPLUS

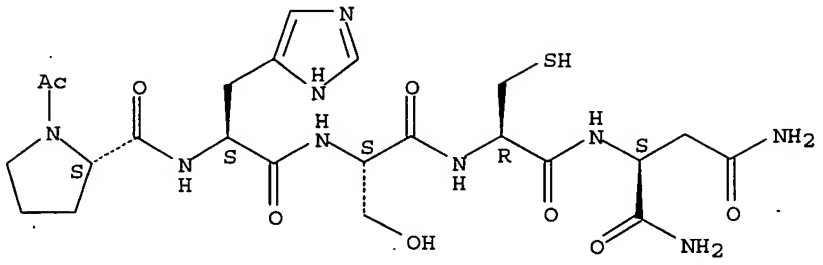
L20 ANSWER 37 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:102218 HCAPLUS
DN 132:245978
TI Anti-invasive, antitumorigenic, and antimetastatic activities of the PHSCN sequence in prostate carcinoma
AU Livant, Donna L.; Brabec, R. Kaye; Pienta, Kenneth J.; Allen, David L.; Kurachi, Kotoku; Markwart, Sonja; Upadhyaya, Ameet
CS Department of Cell and Development Biology, University of Michigan Medical School, Ann Arbor, MI, 48109-0616, USA
SO Cancer Research (2000), 60(2), 309-320
CODEN: CNREA8; ISSN: 0008-5472
PB AACR Subscription Office
DT Journal
LA English
AB Using naturally serum-free SU-ECM basement membranes as invasion substrates showed that plasma fibronectin was necessary to stimulate invasion by DU 145 human and metastatic MATLyLu (MLL) rat prostate carcinoma cells. This activity mapped to the PHSRN sequence, which induced invasion through α5β1 integrin. PHSCN, a competitive inhibitor, blocked both PHSRN- and serum-induced invasion. Acetylated, amidated PHSCN (Ac-PHSCN-NH2) was 30-fold more potent; however, Ac-HSPNC-NH2 was inactive. Rats receiving injections s.c. with 100,000 MLL cells were treated systemically by i.v. injection three times weekly with 1 mg of either Ac-PHSCN-NH2 or Ac-HSPNC-NH2 beginning 24 h later, three times weekly with 1 mg of Ac-PHSCN-NH2 beginning only after surgery to remove large (2 cm) MLL tumors, or were left untreated. MLL tumors grew rapidly in Ac-HSPNC-NH2-treated and in untreated rats. MLL tumor growth in rats treated with Ac-PHSCN-NH2 beginning 1 day after MLL cell injection was reduced by 99.9% during the first 16 days of treatment, although subsequent tumor growth occurred. MLL tumor cryosections immunostained with anti-PECAM-1 showed that Ac-PHSCN-NH2 inhibited neovascularization by 12-fold during this time. Whether initiated after MLL cell injection or only after MLL tumor removal, Ac-PHSCN-NH2 treatment reduced the nos. of MLL lung colonies and micrometastases by 40- to > 100-fold, whereas Ac-HSPNC-NH2 was inactive. Thus, Ac-PHSCN-NH2 may be a potent antitumorigenic and antimetastatic agent for postsurgical use prior to extensive metastasis.
IT **262438-43-7**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(anti-invasive, antitumorigenic, and antimetastatic activities of the PHSCN sequence in prostate carcinoma)

RN 262438-43-7 HCAPLUS
CN L-Aspartamide, 1-acetyl-L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

NTE modified

SEQ 1 PHSCN

Absolute stereochemistry.



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Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Akiyama, S	1995	14	173	Cancer Metastasis Re	HCAPLUS
Akiyama, S	1985	260	4492	J Biol Chem	HCAPLUS
Amemiya, S	1989	31	131	Dev Growth Differ	
Aota, S	1994	269	24756	J Biol Chem	HCAPLUS
Atherton, E	1989			Solid Phase Peptide	
Burnette, W	1981	112	195	Anal Biochem	HCAPLUS
Carter, H	1988		1	A Multidisciplinary	
Clark, R	1996		12	The Molecular and Ce	
de Souza, P	1997	75	1593	Br J Cancer	HCAPLUS
Doherty, D	1990	86	1065	J Clin Invest	HCAPLUS
Dunning, W	1963	12	351	Monogr Natl Cancer I	MEDLINE
Elstein, K	1994	211	322	Exp Cell Res	HCAPLUS
Flaris, N	1993	7	34	GLIA	MEDLINE
Foulkes, E	1991		171	Metallothionein in B	HCAPLUS
Fournier, G	1996	30	32	Eur Urol	
Hayman, E	1979	83	255	J Cell Biol	HCAPLUS
Hayman, E	1982	82	803	Methods Enzymol	
Huhtala, P	1995	129	867	J Cell Biol	HCAPLUS
Humason, G	1972		34	Animal Tissue Techni	
Humphries, M	1986	233	467	Science (Washington	HCAPLUS
Isaacs, J	1986	9	261	Prostate	MEDLINE
Iwamoto, Y	1987	238	1132	Science (Washington	HCAPLUS
Johansson, S	1998	77	1213	Br J Cancer	HCAPLUS
Jungwirth, A	1997	75	1585	Br J Cancer	HCAPLUS
Kim, J	1998	94	353	Cell	HCAPLUS
Lafarga, M	1997	75	137	J Neurosci Methods	HCAPLUS
Litvinovich, S	1995	248	611	J Mol Biol	HCAPLUS
Livant, D	1995	55	5085	Cancer Res	HCAPLUS
Male, D	1995	84	453	Immunology	HCAPLUS
Mant, C	1997	289	426	Methods Enzymol	HCAPLUS
Mogford, J	1997	100	1647	J Clin Investig	HCAPLUS
Mosher, D	1984	35	561	Annu Rev Med	HCAPLUS
Mould, A	1997	272	17283	J Biol Chem	HCAPLUS
Newman, P	1997	100	S25	J Clin Invest	
Peehl, D	1992		159	Culture of Epithelia	
Pienta, K	1995	87	348	J Natl Cancer Inst	HCAPLUS
Pienta, K	1992	20	233	Prostate	HCAPLUS
Pinski, J	1994	54	169	Cancer Res	HCAPLUS
Pinski, J	1993	23	165	Prostate	HCAPLUS

Postlethwaite, A	1976	144	1188	J Exp Med	HCAPLUS
Postlethwaite, A	1981	153	494	J Exp Med	HCAPLUS
Raghaven, D	1988	15	371	Semin Oncol	
Reed, G	1986		313	Manganese in Metabol	HCAPLUS
Roklin, O	1995	26	205	Prostate	
Rossino, P	1990	189	100	Exp Cell Res	HCAPLUS
Saiki, I	1990	81	660	Jpn J Cancer Res	HCAPLUS
Schulze, H	1987	243A	1	Prostate Cancer Part	MEDLINE
Silverberg, E	1988	38	107	CA Cancer J Clin	
Srialovic, G	1990	127	3052	Endocrinology	
Stone, K	1978	21	274	Int J Cancer	MEDLINE
Templeton, N	1990	50	5431	Cancer Res	HCAPLUS
Tomaselli, K	1988	107	1241	J Cell Biol	HCAPLUS
Von Eschenbach, A	1997	47	261	CA Cancer J Clin	MEDLINE
Vukanovic, J	1995	55	1499	Cancer Res	HCAPLUS
Wayner, E	1988	107	1881	J Cell Biol	HCAPLUS
Wiltbank, M	1990	42	139	Biol Reprod	MEDLINE
Witkowski, C	1993	119	637	Cancer Res Clin Onco	HCAPLUS
Zar, J	1984		138	Biostatistical Analy	

L20 ANSWER 38 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:9190 HCAPLUS
DN 132:103595
TI Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
AU Mayer, K.; Schuller, C.; Wambutt, R.; Murphy, G.; Volckaert, G.; Pohl, T.; Dusterhoft, A.; Stiekema, W.; Entlan, K.-D.; Terryn, N.; Harris, B.; Ansorge, W.; Brandt, P.; Grivell, L.; Rieger, M.; Weichselgartner, M.; De Simone, V.; Obermaier, B.; Mache, R.; Muller, M.; Kreis, M.; Delseny, M.; Pulgdomenech, P.; Watson, M.; Schmidtheini, T.; Reichert, B.; Portatelle, D.; Perez-Alonso, M.; Boutry, M.; Bancroft, I.; Vos, P.; Hoheisel, J.; Zimmermann, W.; Wedler, H.; Ridley, P.; Langham, S.-A.; McCullagh, B.; Bilham, L.; Robben, J.; Van Der Schueren, J.; Grymonprez, B.; Chuang, Y.-J.; Vandenbussche, F.; Braeken, M.; Weltjens, I.; Voet, M.; Bastiaens, I.; Aert, R.; Defoor, E.; Weitzenegger, T.; Bothe, G.; Ramsperger, U.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Peters, S.; Van Staveren, M.; Dirkse, W.; Mooijman, P.; Klein Lankhorst, R.; Rose, M.; Haut, J.; Kotter, P.; Berneiser, S.; Hempel, S.; Feldpausch, M.; Lamberth, S.; Van Den Daele, H.; De Keyser, A.; Buysshaert, C.; Gielen, J.; Villarroel, R.; De Clercq, R.; Van Montagu, M.; Rogers, J.; Cronin, A.; Quail, M.; Bray-Allen, S.; Clark, L.; Doggett, J.; Hall, S.; Kay, M.; Lennard, N.; McLay, K.; Mayes, R.; Pettett, A.; Rajandream, M.-A.; Lyne, M.; Benes, V.; Rechmann, S.; Borkova, D.; Blocker, H.; Scharfe, M.; Grimm, M.; Lohnert, T.-H.; Dose, S.; De Haan, M.; Maarse, A.; Schafer, M.; Muller-Auer, S.; Gabel, C.; Fuchs, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Neumann, S.; Argiriou, A.; Vitale, D.; Liguori, R.; Piravandi, E.; Massenet, O.; Quigley, F.; Clabauld, G.; Mundlein, A.; Felber, R.; Schnabl, S.; Hiller, R.; Schmidt, W.; Lecharny, A.; Aubourg, S.; Chefdor, F.; Cooke, R.; Berger, C.; Montfort, M.; Casacuberta, E.; Gibbons, T.; Weber, N.; Vandenbol, M.; Bargues, M.; Terol, J.; Torres, A.; Perez-Perez, A.; Purnelle, B.; Bent, E.; Johnson, S.; Tacon, D.; Jesse, T.; Heijnen, L.; Schwarz, S.; Scholler, P.; Heber, S.; Francs, P.; Bielke, C.; Frishman, D.; Haase, D.; Lemcke, K.; Mewes, H. W.; Stocker, S.; Zaccaria, P.; Bevan, M.; Wilson, R. K.; De La Bastide, M.; Habermann, K.; Parnell, L.; Dedhia, N.; Gnoj, L.; Schutz, K.; Huang, E.; Spiegel, L.; Sehkon, M.; Murray, J.; Sheet, P.; Cordes, M.; Abu-Threideh, J.; Stoneking, T.; Kalicki, J.; Graves, T.; Harmon, G.; Edwards, J.; Latrelle, P.; Courtney, L.; Cloud, J.; Abbott, A.; Scott, K.; Johnson, D.; Minx, P.; Bentley, D.; Fulton, B.; Miller, N.; Greco, T.; Kemp, K.; Kramer, J.; Fulton, L.; Mardis, E.; Dante, M.; Pepin, K.; Hillier, L.; Nelson, J.; Spieth, J.; Ryan, E.; Andrews, S.; Geisel, C.; Layman, D.; Du, H.; Ali, J.; Berghoff, A.; Jones, K.; Drone, K.; Cotton, N.; Joshu, C.; Antonoiu, B.; Zidanic, M.; Strong, C.; Sun, H.; Lamar, B.; Yordan, C.; Ma, P.; Zhong, J.; Preston, R.; Vil, D.; Shekher, M.; Matero, A.; Shah, R.; Swaby, I'K.; O'Shaughnessy, A.; Rodriguez, M.; Hoffman, J.; Till, S.; Granat, S.; Shohdy, N.; Hasegawa, A.; Hameed, A.; Lodhi, M.; Johnson, A.; Chen, E.; Marra, M.; Martienssen, R.; McCombie, W. R.

CS GSF-Forschungszentrum f. Umwelt u. Gesundheit, Munich Information Center for Protein Sequences am Max-Planck-Institut f. Biochemie, D-82152, Germany
SO Nature (London) (1999), 402(6763), 769-777
CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB The higher plant Arabidopsis thaliana is an important model for identifying plant genes and determining their function. To assist biol. investigations and to define chromosome structure, a coordinated effort to sequence the Arabidopsis genome was initiated in late 1996. This report describes one of the first milestones of this project, the sequence of chromosome 4. Anal. of 17.38 megabases of unique sequence, representing about 17% of the genome, reveals 3744 protein coding genes, 81 tRNAs, and numerous repeat elements. Heterochromatic regions surrounding the putative centromere, which has not yet been completely sequenced, are characterized by an increased frequency of a variety of repeats, new repeats, reduced recombination, lowered gene d., and lowered gene expression. Roughly 60% of the predicted protein-coding genes have been functionally characterized on the basis of their homol. to known genes. Many genes encode predicted proteins that are homologous to human and Caenorhabditis elegans proteins.
IT 254859-87-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence and anal. of chromosome 4 of the plant Arabidopsis thaliana)
RN 254859-87-5 HCAPLUS
CN Protein (Arabidopsis thaliana gene T16L4.40) (9CI) (CA INDEX NAME)

SEQ
```
  1 MAKIVILFDF DRTLIDGDSD NWVVTEMGLT EIFHQLRFTL PWNRLMDRMM
 51 MELQSQGRSI DDIKSCLKKM PIDSHIIEAI KSAKSSGCDL KIVSDANQFF
101 IEKILEHHDL VDCFSEIYTN PTSLDDNGNL RILPYHSDAL PPHSCNLCPS
151 NLCKGLVMDH LRASSSNDQI PRRFIYLGDG GGDFCPTLKL RECDFVMPRT
201 NYPLWKKISD NPLLIKAEVK EWSSAEEQQR ILLQLVSTIT KEEDS
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RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Allshire, R	1995	9	218	Genes Dev	HCAPLUS
Altschul, S	1997	25	3389	Nucleic Acids Res	HCAPLUS
Bent, E	1998	13	849	Plant J	HCAPLUS
Bevan, M	1998	391	485	Nature	HCAPLUS
Borodovsky, M	1994	18	259	Comput Chem	HCAPLUS
Bowman, S	1999	400	532	Nature	HCAPLUS
Burge, C	1997	268	78	J Mol Biol	HCAPLUS
Choi, S	1995	2	17	Weeds World	HCAPLUS
Copenhaver, G	1996	9	259	Plant J	HCAPLUS
Copenhaver, G	1996	9	273	Plant J	HCAPLUS
Copenhaver, G	1998	95	247	Proc Natl Acad Sci U	HCAPLUS
Douglas, S	1998	8	655	Curr Opin Genet Dev	HCAPLUS
Emanuelsson, O	1999	8	978	Protein Sci	HCAPLUS
Fichant, G	1991	220	659	J Mol Biol	HCAPLUS
Fransz, P	1998	13	867	Plant J	HCAPLUS
Gamas, P	1996	9	233	Mol Plant Microbe In	HCAPLUS
Gardner, M	1998	282	1126	Science	HCAPLUS
Gerstein, M	1997	274	562	J Mol Biol	HCAPLUS
Grewal, S	1997	146	1221	Genetics	HCAPLUS
Hebsgaard, S	1996	24	3439	Nucleic Acids Res	HCAPLUS
Henning, K	1999	96	592	Proc Natl Acad Sci U	HCAPLUS
Hubbard, T	1999	27	254	Nucleic Acids Res	HCAPLUS

Jensen, R	1998	436	283	FEBS Lett	HCAPLUS
Joazeiro, C	1999	286	309	Science	HCAPLUS
Klein, P	1985	815	468	Biochim Biophys Acta	HCAPLUS
Kotani, H	1997	4	291	DNA Res	HCAPLUS
Lin, X	1999	402	761	Nature	MEDLINE
Lister, C	1993	4	745	Plant J	HCAPLUS
Lupas, A	1991	252	1162	Science	HCAPLUS
Marra, M	1999	22	265	Nature Genet	HCAPLUS
McAinsh, M	1998	3	32	Trends Plant Sci	
Meinke, D	1998	282	662	Science	HCAPLUS
Mewes, H	1997	387	7	Nature	
Mewes, H	1999	27	44	Nucleic Acids Res	HCAPLUS
Mizutani, M	1998	37	39	Plant Mol Biology	HCAPLUS
Moncrief, N	1991	30	522	J Mol Evol	
Mozo, T	1999	22	271	Nature Genet	HCAPLUS
Murphy, T	1995	82	599	Cell	HCAPLUS
Parniske, M	1997	9	821	Cell	
Pearson, W	1988	85	2444	Proc Natl Acad Sci	HCAPLUS
Richards, E	1988	53	127	Cell	HCAPLUS
Richards, E	1998	1	130	Curr Opin Plant Biol	MEDLINE
Richards, E	1991	19	3351	Nucleic Acids Res	HCAPLUS
Round, E	1997	7	1045	Genome Res	HCAPLUS
Schaffer, A				to be published in B	
The C elegans Sequencin	1999	282	2012	Science	
Uberbacher, E	1991	88	1261	Proc Natl Acad Sci	
Vos, P	1995	23	4407	Nucleic Acids Res	HCAPLUS
Wootton, J	1993	17	149	Comput Chem	HCAPLUS
Xu, X	1995	7	2151	Plant Cell	HCAPLUS

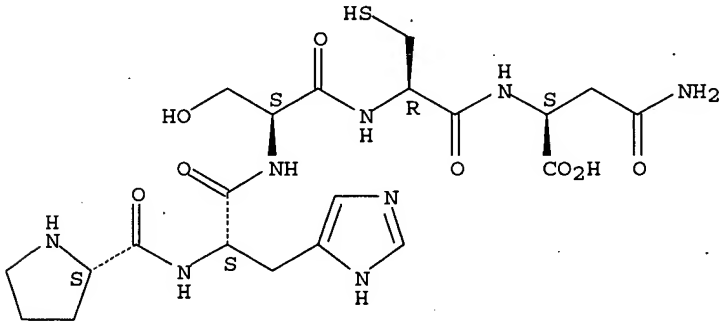
L20 ANSWER 39 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:794362 HCAPLUS
DN 132:30820
TI Anticancer compounds and methods
IN Livant, Donna L.
PA Regents of the University of Michigan, USA
SO U.S., 53 pp., Cont.-in-part of U. S. 5,840,514.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	US---6001965	A	19991214	1997US-0915189	19970820	<--
	US---5840514	A	19981124	1996US-0754322	19961121	<--
	CA---2264570	AA	19980528	1997CA-2264570	19971120	<--
	WO---9822617	A1	19980528	1997WO-US21674	19971120	<--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW					
	RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	EP----928340	A1	19990714	1997EP-0949632	19971120	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
	US---5989850	A	19991123	1998US-0140047	19980826	<--
	US---6472369	B1	20021029	1999US-0373694	19990813	<--
	AU----765126	B2	20030911	2001AU-0051984	20010618	<--
	US2003083264	A1	20030501	2002US-0237850	20020909	<--
	AU2003268832	A1	20040122	2003AU-0268832	20031211	<--
PRAI	1996US-0754322	A2	19961121	<--		
	1997US-0915189	A	19970820	<--		
	1997WO-US21674	W	19971120	<--		
	1999US-0373694	A3	19990813	<--		

2001AU-0051984 A3 20010618 <--
OS MARPAT 132:30820
AB The testing of tumor cells, including human tumors capable of metastases, in assays employing fibronectin-depleted substrates is described. Ex vivo induction of cells, including biopsied human cells, is performed with invasion-inducing agents. Addnl., anti-cancer chemotherapeutics are described. Specifically, chemotherapeutic agents which have anti-metastatic and anti-growth properties are described.
IT **252229-85-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antitumor peptides and inhibition of metastasis)
RN 252229-85-9 HCAPLUS
CN L-Asparagine, L-prolyl-L-histidyl-L-seryl-L-cysteinyl- (9CI) (CA INDEX NAME)

SEQ 1 PHSCN

Absolute stereochemistry.



RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anon	1995			WO---9524471	HCAPLUS
Anon	1996			WO---9612823	HCAPLUS
Aversa	1996			US---5576423	HCAPLUS
Bischoff	1996			US---5539085	HCAPLUS
Bohn	1984			US---4424279	HCAPLUS
Bresalier	1995	55	2476	Cancer Research	HCAPLUS
Burke	1992			US---5169862	HCAPLUS
Calabresi, P			1209	Goodman and Gilman T	
Doersen	1993			US---5264358	
Douillard	1981	II		Compendium of Immuno	
Eldred	1994	37	3882	J Med Chem	HCAPLUS
Gaeta	1996			US---5559103	HCAPLUS
Gartner, T		260	11891	The Journal of Biolo	HCAPLUS
Gerlach, J	1986	5	25	Cancer Surveys	MEDLINE
Ginsberg	1996			US---5523209	HCAPLUS
Ginsburg	1996			US---5492890	HCAPLUS
Goldie, J	1984	44	3643	Cancer Research	HCAPLUS
Hashino	1992			US---5136023	HCAPLUS
Isoai	1996			US---5548062	HCAPLUS
Kitaguchi	1995			US---5436221	HCAPLUS
Kohler, G	1976	6	511	European Journal of	MEDLINE
Kohler, G	1975	256	495	Nature	MEDLINE
Ku	1995	38	9	J Med Chem	HCAPLUS
Lipman, D	1985	227	1435	Science	HCAPLUS

Livant, D	1995	55	5085	Cancer Research	HCAPLUS
Lobl	1993			US---5192746	HCAPLUS
Mennen	1977			US---4018653	HCAPLUS
Nicholson, N	1995	62	567	Thrombosis Research	
Nomizu, M	1993	53	3459	Cancer Research	HCAPLUS
Pearson, W	1988	85	2444	Proc Natl Acad Sci (	HCAPLUS
Reading, C	1982	53	261	Journal of Immunolog	MEDLINE
Saiki, I	1989	49	3815	Cancer Research	HCAPLUS
Schuurs	1977			US---4016043	HCAPLUS
Shashoua	1991			US---5051448	HCAPLUS
Stone, K	1978	21	274	Int J Cancer	MEDLINE
Wenger, R		73	1498	Blood	HCAPLUS

L20 ANSWER 40 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 1996:386154 HCAPLUS
DN 125:56221
TI Cloned transcription factor regulating MHC expression
IN Ono, Santa Jeremy; Strominger, Jack L.
PA Johns Hopkins University, USA; President and Fellows of Harvard College
SO PCT Int. Appl., 92 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO---9612823	A1	19960502	1995WO-US12749	19951020 <--
	W: AL, AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ				
	RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	US---5840832	A	19981124	1994US-0327832	19941021 <--
	AU---9538593	A1	19960515	1995AU-0038593	19951020 <--
	US---5908762	A	19990601	1997US-0828584	19970331 <--
PRAI	1994US-0327832	A	19941021 <--		
	1995WO-US12749	W	19951020 <--		

AB The present invention relates to NF-X1, a novel DNA binding protein which regulates expression of major histocompatibility complex (MHC) class II mols., and to DNA sequences which encode the protein as well as recombinant expression of the protein. NF-X1 is a newly identified, cysteine-rich polypeptide which interacts sequence-specifically with the conserved X1 box regulatory element found in the proximal promoters of class II MHC genes. A cysteine-rich domain within NF-X1 contains a motif repeated seven times, and this entire region is necessary and sufficient for both sequence specific binding and effector function. The motif is related to but distinct from the previously described metal-binding protein families: LIM domain and RING finger. NFX.1 mRNA is markedly overexpressed late after induction of cells with interferon-gamma, and this overexpression coincides with a reduction in the level of HLA-DRA transcript in these cells. Overexpression of this protein strongly and specifically represses the transcription of the HLA-DRA transcript in these cells. Overexpression of this protein strongly and specifically represses the transcription of the HLA-DRA transcript in these cells. Overexpression of this protein strongly and specifically represses the transcription of the HLA-DRA gene in MHC class II pos. cell lines, indicating that the NF-X1 protein is a transcriptional repressor of MHC class II mols. Demonstrated in examples were isolation of cDNA clones encoding NF-X1, primary structure anal. of NF-X1, genomic organization and transcription of NF-X1 gene, NF-X1 encodes a promiscuous X1 box binding protein, delineation of DNA-binding domain of NF-X1, and NF-X1 encodes a repressor of HLA-DRA transcription.

IT **158652-96-1**
RL: BSU (Biological study, unclassified); PRP (Properties); THU

(Therapeutic use); BIOL (Biological study); USES (Uses)
(cloning of transcription factor NF-X1 that regulates expression of antigen MHC class II and interleukin 4)

RN 158652-96-1 HCAPLUS
CN RNA formation factor NF-X 1 (human clone NFX.1cDNA16 nuclear reduced) (9CI) (CA INDEX NAME)

SEQ
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  1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
 51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
151 KPKKATQFVY SYGRGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDQEKCT
301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLICG
701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
751 ECTQTCARVH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
1101 DVQD
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L20 ANSWER 41 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:115603 HCAPLUS
DN 122:125105
TI A novel cysteine-rich sequence-specific DNA-binding protein interacts with the conserved X-box motif of the human major histocompatibility complex class II genes via a repeated Cys-His domain and functions as a transcriptional repressor
AU Song, Zhimin; Krishna, Srikant; Thanos, Dimitris; Strominger, Jack L.; Ono, Santa Jeremy
CS Dep. Med., Johns Hopkins Univ. Sch. Med., Baltimore, MD, 21224, USA
SO Journal of Experimental Medicine (1994), 180(5), 1763-74
CODEN: JEMEAV; ISSN: 0022-1007
DT Journal
LA English
AB The class I major histocompatibility complex (MHC) mols. function in the presentation of processed peptides to helper T cells. As most mammalian cells can endocytose and process foreign antigen, the critical determinant of an antigen-presenting cell is its ability to express class II MHC mols. Expression of these mols. is usually restricted to cells of the immune system and dysregulated expression is hypothesized to contribute to the pathogenesis of a severe combined immunodeficiency syndrome and certain autoimmune diseases. Human complementary DNA clones encoding a newly identified, cysteine-rich transcription factor, NF-X1, which binds to the conserved X-box motif of class II MHC genes, were obtained, and the primary amino acid sequence deduced. The major open reading frame encodes a polypeptide of 1,104 amino acids with a sym. organization. A central cysteine-rich portion encodes the DNA-binding domain, and is subdivided into seven repeated motifs. This motif is similar to but distinct from the LIM domain and the RING finger family, and is reminiscent of known metal-binding regions. The unique arrangement of cysteines indicates that the consensus sequence CX3CXLXCGX1-5HXCX3CHXGXC represents a novel

cysteine-rich motif. Two lines of evidence indicate that the polypeptide encodes a potent and biol. relevant repressor of HLA-DRA transcription: (a) overexpression of NF-X1 from a retroviral construct strongly decreases transcription from the HLA-DRA promoter; and (b) the NF-X1 transcript is markedly induced late after induction with interferon γ (IFN-γ), coinciding with postinduction attenuation of HLA-DRA transcription. The NF-X1 protein may therefore play an important role in regulating the duration of an inflammatory response by limiting the period in which class II MHC mols. are induced by IFN-γ.

IT 158652-96-1, RNA formation factor NF-X1 (human nuclear factor X1)
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(amino acid sequence of; cysteine-rich DNA-binding protein interacts with conserved X-box motif of human major histocompatibility complex class II genes via repeated Cys-His domain and functions as transcriptional repressor)

RN 158652-96-1 HCAPLUS

CN RNA formation factor NF-X 1 (human clone NFX.1cDNA16 nuclear reduced) (9CI) (CA INDEX NAME)

SEQ
```
    1 MEFSSICIEF KSTLRQEAPP PSRAAEPRSS CTVHHLPVTF PGRSLMMKSL
   51 LFISIVIIRQ EGKPKSQQTS FQSSPCNKSP KSHGLQNQPW QKLRNEKHHI
  101 RVKKAQSLAE QTSDTAGLES STRSESGTDL REHSPSESEK EVVGADPRGA
  151 KPKKATQFVY SYGRGPKVKE KLKCEWSNRT TPKPEMLDPK VPNLWGFSTL
  201 TLQRHPLEKE YWMGMEPDEM SREDTHRKGL PGKWRGPGHD QAEIHQNRRA
  251 TDIQTQDTET TWAPFQSDDL NERPAKSTCD SENLAVINKS SRRVDQEKCT
  301 VRRQDPQVVS PFSRGKQNHV LKNVETHTGS LIEQLTTEKY ECMVCCELVR
  351 VTAPVWSCQS CYHVFHLNCI KKWARSPASQ ADGQSGWRCP ACQNVSAHVP
  401 NTFSCFCGKV KNPEWSRNEI PHSCGEVCRK KQPGQDCPHS CNLLCHPGPC
  451 PPCPAFMTKT CECGRTRHTV RCGQAVSVHC SNPCENILNC GQHQCAELCH
  501 GGQCQPCQII LNQVCYCGST SRDVLCGTDV GKSDGFGDFS CLKTCGKDLK
  551 CGNHTCSQVC HPQPCQQCPR LPQLVRCCPC GQTPLSQLLE LGSSSRKTCM
  601 DPVPSCGKVC GKPLPCGSLD FIHTCEKLCH EGDCGPVSRT SVISCRCSFR
  651 TKELPCTSLK SEDATFMCDK RCNKKRLCGR HKCNEICCVD KEHKCPLICG
  701 RKLRCGLHRC EEPCHRGNCQ TCWQASFDEL TCHCGASVIY PPVPCGTRPP
  751 ECTQTCARVH ECDHPVYHSC HSEEKCPPCT FLTQKWCMGK HEFRSNIPCH
  801 LVDISCGLPC SATLPCGMHK CQRLCHKGEC LVDEPCKQPC TTPRADCGHP
  851 CMAPCHTSSP CPVTACKAKV ELQCECGRRK EMVICSEASS TYQRIAAISM
  901 ASKITDMQLG GSVEISKLIT KKEVHQARLE CDEECSALER KKRLAEAFHI
  951 SEDSDPFNIR SSGSKFSDSL KEDARKDLKF VSDVEKEMET LVEAVNKGKN
 1001 SKKSHSFPPM NRDHRRIIHD LAQVYGLESV SYDSEPKRNV VVTAIRGKSV
 1051 CPPTTLTGVL EREMQARPPP PIPHHRHQSD KNPGSSNLQK ITKEPIIDYF
 1101 DVQD
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L20 ANSWER 42 OF 42 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 1986:103366 HCAPLUS

DN 104:103366

TI Analysis of cloned cDNA and genomic sequences for phytochrome: complete amino acid sequences for two gene products expressed in etiolated Avena

AU Hershey, Howard P.; Barker, Richard F.; Idler, Kenneth B.; Lissemore, James L.; Quail, Peter H.

CS Dep. Bot., Univ. Wisconsin, Madison, WI, 53706, USA

SO Nucleic Acids Research (1985), 13(23), 8543-59
CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Cloned cDNA and genomic sequences were analyzed to deduce the amino acid sequence of phytochrome of etiolated Avena. Restriction endonuclease site polymorphism between clones indicates that ≥4 phytochrome genes are expressed in this tissue. Sequence anal. of 2 complete and 1 partial coding region shows .apprx.98% homol. at both the nucleotide and amino

acid levels, with the majority of amino acid changes being conservative. High sequence homol. is also found in the 5'-untranslated region but significant divergence occurs in the 3'-untranslated region. The phytochrome polypeptides are 1128-amino acid residues long corresponding to a mol. mass of 125 kilodaltons. The known protein sequence at the chromophore attachment site occurs only once in the polypeptide, establishing that phytochrome has a single chromophore per monomer covalently linked to Cys-321. Computer analyses of the amino acid sequences have provided predictions regarding a number of structural features of the phytochrome mol.

IT **100469-69-0 100469-70-3**
RL: PRP (Properties)
(amino acid sequence of)

RN 100469-69-0 HCAPLUS
CN Phytochrome (oat clone λ2.4 subunit protein moiety reduced) (9CI) (CA INDEX NAME)

SEQ
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      1 MSSSRPASSS SSRNRQSSRA RYLAQTTLDA ELWAEYEESG DSFDYSKLVE
     51 AQRDGPPVQQ GRSEKVIAYL QHIGKGKLIG TFFGCNLALD EKSFNVIAFS
    101 ENAPEMLTTV SNAVPSVDDP PRLGIGTNYR SLFSDQFATA LNKALGFADY
    151 SLLNPILVGC KTSGKPFYAI VHRATGCLVV DFEPYKPTEF PATAAGALQS
    201 YKLAAKAISK IGSLPGGSME VLCMTYYKEV FDLTGYDRVM AYKFMEDDMG
    251 FYFAEITKPG LPYLGLNYPA TDIPGAARFL FRKNKVRMIC DCRARSIKYI
    301 EAEALPFDIS LCGSALRAPH SCNLQYRENA NSIASLYRAY YYMEMEEDDE
    351 AESEQPAQQQ QKKKLWELLV CNHESPRTYP FPLRYACEFL AQVFAYHYHR
    401 EFELEKGLRE KSILKHQTRL SDMLFREASP LTIYSRAPHI MDEYKCDGAA
    451 LLTGGKYYGT PPPAPTFSQL HDIAFWLSDV NRDSYGLSYD SLHDAGYPGA
    501 SAGDAICGAA YAKINSDKII FWFRSNTAAE IRWGGAKHDS SDADDSRRMH
    551 PRISFKAFLF YYKAKSLPVT DYEMDAINSL QLILRGTLND ASKPKREASL
    601 DMQIGDLKLD GLAFLQAYTS EMVRLMFTAT VPILAVDGMG LVMGMMGKAA
    651 ELTGLRVDDA IGRHILTLVE ESSYPVVQRM LYLALQGKEE KEYRFEYKTH
    701 GPKRDDGPYI LYYHACASRD LNDNYVGYCF YAGDATVNKL VADKFTRYEG
    751 DTKAIINNPN PLIPPIFGAD FFGNCSEWNA AMTKLTGWNR DEYLDERLLG
    801 EVFDSSNASC PLKNKNAFYS LCYLINSALA GEETEKAPFG FFPSGKTIEC
    851 LLSANRKENE GGLITGYFCF INYASNELQN ALGYGQASEQ TSLKRLKAFS
    901 YRRHAINNPL ASGNLYSRKA LKNTPLWEEG NKQINYGDNC HNGINKILAD
    951 LDGDSISEKS SCLDLFMAFF VFGDVVVAAV SGYLIICGGK GIRISCHLPE
   1001 RFMKQSVYGD GVRLGGILSD FLFISYKFSP VFFSVEISSK LTKMSIGENL
   1051 NLIDLELRIK NGGLGYPAEL MEGMFEEDMK EGSDEGLGLL VSRKLLRLRN
   1101 GDVRNLREAG VSTFLLTAEL ASAPTAIGQ
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RN 100469-70-3 HCAPLUS
CN Phytochrome (oat clone λ8.2 subunit protein moiety reduced) (9CI) (CA INDEX NAME)

SEQ
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      1 MSSSRPASSS SSRNRQSSQA RVLAQTTLDA ELWAEYEESG DSFDYSKLYE
     51 AQRDGPPYQQ GRESEKYIAT LQNIQKEGKL IGTFGCLLAL DEKSFNVIAF
    101 SENAPEMLTT VSNAVPSVDD PPRLGIGTNV RSLFSDQGAT ALNKALGFAD
    151 YSLLNPILYQ CKTSGKPFTA IYNRATGCLV VDFEPVKPTE FATAAGALGS
    201 TKLAAKAISK LQSLLPGGSM EYLCNTYYKE YFDLTGTDRY MAYKFNEDDH
    251 GEYFSEITKP GLEPTLGLMY PATDIPQAAR LLGMKNEYRR ICDCRARSIK
    301 YIEAELPFDI SLCGSALRPH SCNLQYMENN HSIASLYRAV VVHEMEEDDE
    351 AESEQPAQQQ KKKKLWGLLY CHHESPRYVP FPLRYACEFL AQVFAVHVNR
    401 EFELEKQLRE KNILKMQTAM LSDMLFREAS PLTIVSGTPN IMDEVKCDGA
    451 ALLYGGKVMR LRMAPTESQI HDISFWLSDV HRDSTGLSTD SLHDAGYPGA
    501 AALGDMICGM AVAKIMSKDI LFWFRSHTAA EIRWGGAKND PSDMDDSRRM
    551 HPRLSFKAFL FVVKMKSLPM SDYEMDAINS LQLILRGTLN DASKPKREAS
    601 LDNGIGDLKL DGLAFLQAVT SEMVRLMETA TVPILAVDGN GLVNGVHQKA
    651 AELTGLRVDD AIGRHILTLV EDSSYPVYQR RLYLALQGKE FDEYRFEVKT
    701 HGPKRDDGPV ILVVNACASR DLNDHVVGVC GVCFVAWDMT VHKLVRDKFT
    751 RVEGDYKAII HMPHPLIPPI FGADEFGMCS EWNAAMTKLT GVMRDFVLDE
    801 ALLGEYGSSM ASCPLKHRDA FVSLCVLIHS ALAGEETEKA PFGFFDRSGK
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 851 YIECLLSAHR KEMEGGLITG VFCFINYASN ELGNALQVQQ ASEQTSLKRL
 901 KAFSYARHAI HHPLSGRLYS RKALKMTDLN EEQRKQINYG DACMMGINKI
 951 LADLDGDSIT EKSSCLDLSM AEFLLGDYYV AAYSQYLITC QGKGIRISCM
1001 LPERFMKQSV YGDGVRLQQI LSFLFISVKF SPYGGSVEIS SKLTKMSIGE
1051 NLNLIDLELR IKHQGLGVPA ELMAQMGEED MKEQSEEGLS LLYSRNLLRL
1101 MNGDYRHLRE AGYSTFIITA ELASAPTAMG Q
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                 E ALLAN A/AU
L3            36 E3,E11
                 E ALLAN AMY/AU
L4             6 E5
                 E GLADSTONE P/AU
L5            28 E3-7
                 E PARRY G/AU
L6           181 E3-14
                 E PARRY GRAHAM/AU
L7            43 E3-5
                 E DONATE F/AU
L8            28 E3-4,E6
                 E MAZAR A/AU
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L10           23 ATTENUON/PA,CS

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